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|---|---|---|
| NEWS 1 | | Web Page URLs for STN Seminar Schedule - N. America |
| NEWS 2 | Jan 25 | BLAST(R) searching in REGISTRY available in STN on the Web |
| NEWS 3 | Jan 29 | FSTA has been reloaded and moves to weekly updates |
| NEWS 4 | Feb 01 | DKILIT now produced by FIZ Karlsruhe and has a new update frequency |
| NEWS 5 | Feb 19 | Access via Tymnet and SprintNet Eliminated Effective 3/31/02 |
| NEWS 6 | Mar 08 | Gene Names now available in BIOSIS |
| NEWS 7 | Mar 22 | TOXLIT no longer available |
| NEWS 8 | Mar 22 | TRCTHERMO no longer available |
| NEWS 9 | Mar 28 | US Provisional Priorities searched with P in CA/CAplus and USPATFULL |
| NEWS 10 | Mar 28 | LIPINSKI/CALC added for property searching in REGISTRY |
| NEWS 11 | Apr 02 | PAPERCHEM no longer available on STN. Use PAPERCHEM2 instead. |
| NEWS 12 | Apr 08 | "Ask CAS" for self-help around the clock |
| NEWS 13 | Apr 09 | BEILSTEIN: Reload and Implementation of a New Subject Area |
| NEWS 14 | Apr 09 | ZDB will be removed from STN |
| NEWS 15 | Apr 19 | US Patent Applications available in IFICDB, IFIPAT, and IFIUDB |
| NEWS 16 | Apr 22 | Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS |
| NEWS 17 | Apr 22 | BIOSIS Gene Names now available in TOXCENTER |
| NEWS 18 | Apr 22 | Federal Research in Progress (FEDRIP) now available |

| | |
|---|---|
| NEWS EXPRESS | February 1 CURRENT WINDOWS VERSION IS V6.0d, CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP), AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002 |
| NEWS HOURS | STN Operating Hours Plus Help Desk Availability |
| NEWS INTER | General Internet Information |
| NEWS LOGIN | Welcome Banner and News Items |
| NEWS PHONE | Direct Dial and Telecommunication Network Access to STN |
| NEWS WWW | CAS World Wide Web Site (general information) |

Enter NEWS followed by the item number or name to see news on that specific topic.

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FILE 'HOME' ENTERED AT 08:40:32 ON 03 MAY 2002

=> FIL BIOSIS MEDLINE SCISEARCH CA

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COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
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FULL ESTIMATED COST                                        0.42        0.42

FILE 'BIOSIS' ENTERED AT 08:41:51 ON 03 MAY 2002
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FILE 'MEDLINE' ENTERED AT 08:41:51 ON 03 MAY 2002

FILE 'SCISEARCH' ENTERED AT 08:41:51 ON 03 MAY 2002
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=> s eif2? or co-eif? or (eukaryotic (3n) initiation (3n) factor)
L1         7142 EIF2? OR CO-EIF? OR (EUKARYOTIC (3N) INITIATION (3N) FACTOR)

=> s antisense or (complement? (3n) (seauenc? or oligo?))
L2        81699 ANTISENSE OR (COMPLEMENT? (3N) (SEAUENC? OR OLIGO?))

=> s l1 and l2
L3           83 L1 AND L2

=> s l3 and inhib?
<------User Break------>
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SEARCH ENDED BY USER

=> s l3 and (inhib? or reduc? or prevent? or lower? or suppress?) (3n) express?
   2 FILES SEARCHED...
L4            2 L3 AND (INHIB? OR REDUC? OR PREVENT? OR LOWER? OR SUPPRESS?)
                (3N) EXPRESS?

=> s antisense or (complement? (3n) (sequenc? or oligo?))
L5       127625 ANTISENSE OR (COMPLEMENT? (3N) (SEQUENC? OR OLIGO?))

=> s l1 and l5
L6          150 L1 AND L5

=> s l6 and (inhib? or reduc? or prevent? or lower? or suppress?) (3n) express?
   2 FILES SEARCHED...
L7            2 L6 AND (INHIB? OR REDUC? OR PREVENT? OR LOWER? OR SUPPRESS?)
                (3N) EXPRESS?

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     (FILE 'HOME' ENTERED AT 08:40:32 ON 03 MAY 2002)

     FILE 'BIOSIS, MEDLINE, SCISEARCH, CA' ENTERED AT 08:41:51 ON 03 MAY 2002
L1         7142 S EIF2? OR CO-EIF? OR (EUKARYOTIC (3N) INITIATION (3N) FACTOR)
L2        81699 S ANTISENSE OR (COMPLEMENT? (3N) (SEAUENC? OR OLIGO?))
L3           83 S L1 AND L2
L4            2 S L3 AND (INHIB? OR REDUC? OR PREVENT? OR LOWER? OR SUPPRESS?)
L5       127625 S ANTISENSE OR (COMPLEMENT? (3N) (SEQUENC? OR OLIGO?))
L6          150 S L1 AND L5
L7            2 S L6 AND (INHIB? OR REDUC? OR PREVENT? OR LOWER? OR SUPPRESS?)

=> d l7 1-2 bib abs
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L7 ANSWER 1 OF 2 CA COPYRIGHT 2002 ACS
AN 129:258972 CA
TI Identification of tumor-associated alleles of genes essential for cell viability and growth and the development of neoplasm inhibitors targeted against them
IN Housman, David; Ledley, Fred D.; Stanton, Vincent P., Jr.
PA Variagenics, Inc., USA
SO PCT Int. Appl., 605 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|---|
| PI | WO 9841648 | A2 | 19980924 | WO 1998-US5419 | 19980319 |
| | WO 9841648 | A3 | 19990429 | | |
| | W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW | | | | |
| | RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| | AU 9867643 | A1 | 19981012 | AU 1998-67643 | 19980319 |
| | EP 973935 | A2 | 20000126 | EP 1998-912974 | 19980319 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI | | | | |
| PRAI | US 1997-41057P | P | 19970320 | | |
| | WO 1998-US5419 | W | 19980319 | | |

AB Strategies for the identification and targeting of specific alleles of genes in the treatment of tumors are described. Tumor-assocd. alleles of genes coding for proteins essential for cell viability or cell growth and that show loss of an alleles in cancer cells due to loss of heterozygosity (LOH) are identified. Inhibitors of the remaining allele, such as **antisense** nucleic acids or ribozymes, can then be developed. The method can also be used to **inhibit** the **expression** of particular alleles of genes for antigens in the control of transplant rejection. Particular categories of appropriate target genes are described, along with specific exemplary genes within those categories and methods of using such target genes. **Antisense** phosphorothioate oligonucleotides targeting RNA polymerase II and glutamyl/prolyl tRNA synthetase genes were tested for cytotoxicity in vitro. Oligonucleotides with a single base mismatch were significantly less toxic than those without mismatches. A no. of genes essential for proliferation were mapped and shown to be affected by loss-of-heterozygosity in oncogenesis.

L7 ANSWER 2 OF 2 CA COPYRIGHT 2002 ACS
AN 127:157618 CA
TI Compositions and methods for modulating RNA activity through modification of the 5' cap structure of RNA
IN Baker, Brenda F.
PA ISIS Pharmaceuticals, Inc., USA
SO U.S., 19 pp. Cont.-in-part of U.S. Ser. No. 847,054, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|---|
| PI | US 5643780 | A | 19970701 | US 1994-327363 | 19941021 |
| PRAI | US 1992-847054 | | 19920403 | | |

AB Methods for regulating gene expression in biol. exptl. systems via modification or removal of the 5' cap structure of targeted RNAs are

disclosed. Modification or removal of the 5' cap structure is achieved in accordance with preferred embodiments utilizing **antisense** compds. which are complementary to the 5' terminus of the targeted RNA and have attached to them reactive moieties explicitly designed for chem. modification or cleavage of the 5' cap structure of RNA. Thus, the 5' capped RNA target m7GpppGAGCUCCUCUGCUACUCAGA32pCp and the **antisense** oligodeoxyribonucleotide TCTGAGTAGCAGAGGAGCTCGGT were synthesized; reactive moieties such as Cu(II)-N-(2-mercaptoacetyl)glutamine or Cu(II)-N-(2-mercaptopropionyl)glycine were tethered to the 3'-terminus of the **antisense** oligonucleotide. The **antisense** oligonucleotide inhibits complexation of **eukaryotic initiation factor** 4E protein to the mRNA target by cleaving the 5'-cap. Other tethered mols. were also found to **inhibit** gene **expression** at the mRNA level, such as alkyl amines (triethylene tetramine), arom. amines (imidazole), and lanthamide metal coordination complexes (Eu:DTPA-dien). Compns. that have utility as research reagents and therapeutics for the treatment of diseases are disclosed.

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| NEWS 2 | | "Ask CAS" for self-help around the clock |
| NEWS 3 | Feb 24 | PCTGEN now available on STN |
| NEWS 4 | Feb 24 | TEMA now available on STN |
| NEWS 5 | Feb 26 | NTIS now allows simultaneous left and right truncation |
| NEWS 6 | Feb 26 | PCTFULL now contains images |
| NEWS 7 | Mar 04 | SDI PACKAGE for monthly delivery of multifile SDI results |
| NEWS 8 | Mar 24 | PATDPAFULL now available on STN |
| NEWS 9 | Mar 24 | Additional information for trade-named substances without structures available in REGISTRY |
| NEWS 10 | Apr 11 | Display formats in DGENE enhanced |
| NEWS 11 | Apr 14 | MEDLINE Reload |
| NEWS 12 | Apr 17 | Polymer searching in REGISTRY enhanced |
| NEWS 13 | AUG 15 | Indexing from 1937 to 1946 added to records in CA/CAPLUS |
| NEWS 14 | Apr 21 | New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX |
| NEWS 15 | Apr 28 | RDISCLOSURE now available on STN |
| NEWS 16 | May 05 | Pharmacokinetic information and systematic chemical names added to PHAR |
| NEWS 17 | May 15 | MEDLINE file segment of TOXCENTER reloaded |
| NEWS 18 | May 15 | Supporter information for ENCOMPPAT and ENCOMPLIT updated |
| NEWS 19 | May 19 | Simultaneous left and right truncation added to WSCA |
| NEWS 20 | May 19 | RAPRA enhanced with new search field, simultaneous left and right truncation |
| NEWS 21 | Jun 06 | Simultaneous left and right truncation added to CBNB |
| NEWS 22 | Jun 06 | PASCAL enhanced with additional data |
| NEWS 23 | Jun 20 | 2003 edition of the FSTA Thesaurus is now available |
| NEWS 24 | Jun 25 | HSDB has been reloaded |
| NEWS 25 | Jul 16 | Data from 1960-1976 added to RDISCLOSURE |
| NEWS 26 | Jul 21 | Identification of STN records implemented |
| NEWS 27 | Jul 21 | Polymer class term count added to REGISTRY |
| NEWS 28 | Jul 22 | INPADOC: Basic index (/BI) enhanced; Simultaneous Left and Right Truncation available |
| NEWS 29 | AUG 05 | New pricing for EUROPATFULL and PCTFULL effective August 1, 2003 |
| NEWS 30 | AUG 13 | Field Availability (/FA) field enhanced in BEILSTEIN |
| NEWS 31 | AUG 15 | PATDPAFULL: one FREE connect hour, per account, in September 2003 |
| NEWS 32 | AUG 15 | PCTGEN: one FREE connect hour, per account, in September 2003 |
| NEWS 33 | AUG 15 | RDISCLOSURE: one FREE connect hour, per account, in September 2003 |
| NEWS 34 | AUG 15 | TEMA: one FREE connect hour, per account, in September 2003 |

NEWS EXPRESS April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT

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                MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
                AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
 NEWS HOURS     STN Operating Hours Plus Help Desk Availability
 NEWS INTER     General Internet Information
 NEWS LOGIN     Welcome Banner and News Items
 NEWS PHONE     Direct Dial and Telecommunication Network Access to STN
 NEWS WWW       CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 12:31:12 ON 16 AUG 2003

=> FIL MEDLINE BIOSIS EMBASE CA SCISEARCH
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

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FILE 'BIOSIS' ENTERED AT 12:31:17 ON 16 AUG 2003
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=> s (eukaryot? (n) translation? (n) factor (n) 2c?) or (co (n) eif (n) 2c?) or
eif2c or (golgi (n) er (n) protein? (n) 95 (n) (kd?)) or gerp95 or q99)
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The number of right parentheses in a query must be equal to the
number of left parentheses.

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eif2c or (golgi (n) er (n) protein? (n) 95 (n) (kd?)) or gerp95 or q99
   4 FILES SEARCHED...
L1          107 (EUKARYOT? (N) TRANSLATION? (N) FACTOR (N) 2C?) OR (CO (N) EIF
                (N) 2C?) OR EIF2C OR (GOLGI (N) ER (N) PROTEIN? (N) 95 (N) (KD?)
                ) OR GERP95 OR Q99

=> s antisense or rnai or (anti (n) sense) or (complement? (2n) (oligonucl? or
nucl?))
L2       130563 ANTISENSE OR RNAI OR (ANTI (N) SENSE) OR (COMPLEMENT? (2N) (OLIG
                ONUCL? OR NUCL?))

=> s l1 and l2
L3           16 L1 AND L2
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=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 6 DUP REM L3 (10 DUPLICATES REMOVED)

=> d l4 1-6 ibib abs

L4 ANSWER 1 OF 6 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2003020539 IN-PROCESS
DOCUMENT NUMBER: 22414943 PubMed ID: 12526743
TITLE: Short-interfering-RNA-mediated gene silencing in mammalian cells requires Dicer and **eIF2C** translation initiation factors.
AUTHOR: Doi Noboru; Zenno Shuhei; Ueda Ryu; Ohki-Hamazaki Hiroko; Ui-Tei Kumiko; Saigo Kaoru
CORPORATE SOURCE: Department of Biophysics, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, 113-0033, Bunkyo-ku, Tokyo, Japan.
SOURCE: CURRENT BIOLOGY, (2003 Jan 8) 13 (1) 41-6.
Journal code: 9107782. ISSN: 0960-9822.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
OTHER SOURCE: GDB-AB028449; GENBANK-AB046787; GENBANK-AB081470; GENBANK-AB081471; GENBANK-AB081472; GENBANK-AB081473; GENBANK-AB081474
ENTRY DATE: Entered STN: 20030116
Last Updated on STN: 20030715

AB RNA interference (**RNAi**) is the process of long, double-stranded (ds), RNA-dependent posttranscriptional gene silencing (PTGS). In lower eukaryotes, dsRNA introduced into the cytoplasm is cleaved by the RNaseIII-like enzyme, Dicer, to 21-23 nt RNA (short interfering [si] RNA), which may serve as guide for target mRNA degradation. In mammals, long-dsRNA-dependent PTGS is applicable only to a limited number of cell types, whereas siRNA synthesized in vitro is capable of effectively inducing gene silencing in a wide variety of cells. Although biochemical and genetic analyses in lower eukaryotes showed that Dicer and some PIWI family member proteins are essential for long-dsRNA-dependent PTGS, little is known about the molecular mechanisms underlying siRNA-based PTGS. Here, we show that Dicer and **eIF2C** translation initiation factors belonging to the PIWI family (eIF2C1-4) play an essential role in mammalian siRNA-mediated PTGS, most probably through synergistic interactions. Immunoprecipitation experiments suggest that, in human and mouse cells, complex formation occurs between Dicer and eIF2C1 or 2 and that the PIWI domain of **eIF2C** is essential for the formation of this complex.

L4 ANSWER 2 OF 6 CA COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 139:80222 CA
TITLE: Protein and cDNA sequences of 21.56-kilodalton human initiation factor **eIF2C**-like protein and their therapeutic uses
INVENTOR(S): Mao, Yumin; Xie, Yi
PATENT ASSIGNEE(S): Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 32 pp.
CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| CN 1363568 | A | 20020814 | CN 2001-105038 | 20010105 |

PRIORITY APPLN. INFO.: CN 2001-105038 20010105

AB The invention provides protein and cDNA sequences of a novel 21.56-kilodalton human protein, designated as "initiation factor **eIF2C** 21.56", which has similar expression pattern to that of known initiation factor **eIF2C**. The invention relates to expression of initiation factor **eIF2C**-like protein in E. coli BL21(DE3)plySs transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against initiation factor **eIF2C** -like protein. The invention further relates to the uses of the initiation factor **eIF2C**-like protein in treatment of initiation factor **eIF2C**-related diseases (such as neoplasm, blood disease, HIV infection, immune disease, inflammation, etc).

L4 ANSWER 3 OF 6 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 2002470265 MEDLINE
DOCUMENT NUMBER: 22217361 PubMed ID: 12230974
TITLE: Single-stranded **antisense** siRNAs guide target RNA cleavage in **RNAi**.
AUTHOR: Martinez Javier; Patkaniowska Agnieszka; Urlaub Henning; Luhrmann Reinhard; Tuschl Thomas
CORPORATE SOURCE: Department of Cellular Biochemistry, Max-Planck-Institute for Biophysical Chemistry, Am Fassberg 11, D-37077, Gottingen, Germany.
SOURCE: CELL, (2002 Sep 6) 110 (5) 563-74.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200302
ENTRY DATE: Entered STN: 20020917
Last Updated on STN: 20030207
Entered Medline: 20030206

AB Small interfering RNAs (siRNAs) are the mediators of mRNA degradation in the process of RNA interference (**RNAi**). Here, we describe a human biochemical system that recapitulates siRNA-mediated target RNA degradation. By using affinity-tagged siRNAs, we demonstrate that a single-stranded siRNA resides in the RNA-induced silencing complex (RISC) together with eIF2C1 and/or eIF2C2 (human **GERp95**) Argonaute proteins. RISC is rapidly formed in HeLa cell cytoplasmic extract supplemented with 21 nt siRNA duplexes, but also by adding single-stranded **antisense** RNAs, which range in size between 19 and 29 nucleotides. Single-stranded **antisense** siRNAs are also effectively silencing genes in HeLa cells, especially when 5'-phosphorylated, and expand the repertoire of RNA reagents suitable for gene targeting.

L4 ANSWER 4 OF 6 CA COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 134:336728 CA
TITLE: Protein and cDNA sequences of a novel human protein formation initiation factor 28 and diagnostic and therapeutic uses thereof
INVENTOR(S): Mao, Yumin; Xie, Yi
PATENT ASSIGNEE(S): Shanghai Bio Road Gene Development Ltd., Peop. Rep. China
SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Chinese

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2001031001 | A1 | 20010503 | WO 2000-CN382 | 20001027 |

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

| | | | | |
|---|---|---|---|---|
| CN 1302874 | A | 20010711 | CN 1999-119888 | 19991028 |

PRIORITY APPLN. INFO.: CN 1999-119888 A 19991028

AB The invention provides protein and cDNA sequences for a novel human protein formation initiation factor 28, which shares sequence homol. with rabbit protein formation initiation factor **eIF2C**. The invention also relates to constructs and methods to express the cloned gene for the prepn. of its protein and antibodies using E.coli cells or eukaryotic cells, and diagnostic and therapeutic uses for protein formation initiation factor 28 related diseases.

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3

ACCESSION NUMBER: 2001:557226 BIOSIS
DOCUMENT NUMBER: PREV200100557226
TITLE: PTGS in plants, a virus resistance mechanism. Original Title: L'inactivation epigenetique post-transcriptionnelle chez les vegetaux: Un mecanisme de resistance aux virus..
AUTHOR(S): Beclin, Christophe (1); Vaucheret, Herve
CORPORATE SOURCE: (1) Laboratoire de Biologie Cellulaire, UR 501, INRA, 78026, Versailles Cedex: beclin@versailles.inra.fr, vauchere@versailles.inra.fr France
SOURCE: M-S (Medecine Sciences), (Septembre, 2001) Vol. 17, No. 8-9, pp. 845-855. print.
ISSN: 0767-0974.
DOCUMENT TYPE: General Review
LANGUAGE: French
SUMMARY LANGUAGE: English; French

AB Post-transcriptional gene silencing (PTGS) in plants and quelling in fungi are transgene-induced silencing phenomena, resulting from the degradation of transgene RNAs and homologous endogenous RNAs. PTGS shows similarities with **RNAi** in animals, a phenomenon induced by injection of double-stranded RNA (dsRNA) or introduction of transgenes expressing dsRNA. First, PTGS and **RNAi** both involve dsRNA. Second, they can be dissected into three steps: localized initiation, propagation of a sequence-specific systemic signal, maintenance in silenced tissues. Finally, they both correlate with the accumulation of 25nt sense and **anti-sense** RNAs. Genetic dissection and cloning of genes regulating PTGS, quelling and **RNAi** confirmed the links between these three phenomena. Indeed, all three involve a putative RNA-dependent-RNA polymerase and a protein similar to the translation initiator factor **eIF2C**. However some differences can be noticed. In particular, PTGS in plants requires two genes, SGS3 (encoding a protein of unknown function) and MET1 (encoding a DNA-methyltransferase), which are not required for **RNAi**. Indeed, the genomes of C. elegans and

Drosophila (two organisms undergoing **RNAi**) lack both methylation and orthologs of the SGS3 gene). Several experiments revealed that PTGS is a general mechanism of virus resistance. In particular, we showed that Arabidopsis mutants impaired in PTGS are hypersensitive to infection by the virus CMV. However, many viruses have developed strategies to counteract PTGS and therefore succeed to infect plants. Because viruses may act as targets, inducers or inhibitors of PTGS, the success and the extent of virus infection therefore depends on the competition between plant PTGS defenses and virus counteracting effects.

L4 ANSWER 6 OF 6 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2000004389 MEDLINE
DOCUMENT NUMBER: 20004389 PubMed ID: 10535731
TITLE: The rde-1 gene, RNA interference, and transposon silencing in C. elegans.
AUTHOR: Tabara H; Sarkissian M; Kelly W G; Fleenor J; Grishok A; Timmons L; Fire A; Mello C C
CORPORATE SOURCE: Department of Cell Biology, Program in Molecular Medicine, University of Massachusetts Cancer Center, Worcester 01605, USA.
CONTRACT NUMBER: GM37706 (NIGMS)
GM58800 (NIGMS)
HD08353 (NICHD)
SOURCE: CELL, (1999 Oct 15) 99 (2) 123-32.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF180730
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991110
AB Double-stranded (ds) RNA can induce sequence-specific inhibition of gene function in several organisms. However, both the mechanism and the physiological role of the interference process remain mysterious. In order to study the interference process, we have selected C. elegans mutants resistant to dsRNA-mediated interference (**RNAi**). Two loci, rde-1 and rde-4, are defined by mutants strongly resistant to **RNAi** but with no obvious defects in growth or development. We show that rde-1 is a member of the piwi/sting/argonaute/zwille/**eIF2C** gene family conserved from plants to vertebrates. Interestingly, several, but not all, **RNAi**-deficient strains exhibit mobilization of the endogenous transposons. We discuss implications for the mechanism of **RNAi** and the possibility that one natural function of **RNAi** is transposon silencing.

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(FILE 'HOME' ENTERED AT 12:31:12 ON 16 AUG 2003)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 12:31:17 ON 16 AUG 2003
L1 107 S (EUKARYOT? (N) TRANSLATION? (N) FACTOR (N) 2C?) OR (CO (N) EI
L2 130563 S ANTISENSE OR RNAI OR (ANTI (N) SENSE) OR (COMPLEMENT? (2N) (O
L3 16 S L1 AND L2
L4 6 DUP REM L3 (10 DUPLICATES REMOVED)

=> s l1 (3n) inhib?
L5 8 L1 (3N) INHIB?

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6 3 DUP REM L5 (5 DUPLICATES REMOVED)

=> d l6 1-3 ibib abs

L6 ANSWER 1 OF 3 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 83065205 MEDLINE
DOCUMENT NUMBER: 83065205 PubMed ID: 6959132
TITLE: Protein synthesis in rabbit reticulocytes: characteristics of the protein factor RF that reverses inhibition of protein synthesis in heme-deficient reticulocyte lysates.
AUTHOR: Grace M; Ralston R O; Banerjee A C; Gupta N K
CONTRACT NUMBER: 18796 (NIGMS)
GM 22079 (NCRR)
RR 07055
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1982 Nov) 79 (21) 6517-21. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198301
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19970203
Entered Medline: 19830127

AB During heme deficiency in reticulocyte lysates, the heme-regulated translational inhibitor of protein synthesis (HRI) is activated and shuts off protein synthesis. In partial reactions, HRI phosphorylates the Mr 38,000 subunit (alpha subunit) of eukaryotic initiation factor 2 (eIF-2), which forms a ternary complex, Met-tRNAf X eIF-2 X GTP. The eIF-2 alpha (P) thus formed is not recognized by two eIF-2 ancillary factors, Co-eIF-2B (which promotes the dissociation of the ternary complex at high Mg2+) and **Co-eIF-2C** (which reverses the **inhibition** of ternary complex formation), and thus, is presumably inactive in peptide chain initiation. A protein factor, designated RF, which reverses inhibition of protein synthesis in heme-deficient reticulocyte lysates, has been purified from reticulocyte cell supernatant. RF is a high molecular weight (Mr approximately equal to 450,000) protein complex composed of multiple polypeptides. An active RF preparation contains Co-eIF-2B and Co-eIF-2C activities, and these two activities in RF preparation are not inhibited by HRI and ATP--i.e., eIF-2 alpha (P) is recognized. During purification, RF remains associated with eIF-2 activity (eIF-2 X RF) and can be freed of this eIF-2 activity by CM-Sephadex chromatography. Both eIF-2 X RF and RF contain a Mr 38,000 polypeptide component that is indistinguishable from the Mr 38,000 subunit of eIF-2 by two-dimensional gel electrophoresis. It has been observed that a significant part of this Mr 38,000 polypeptide component in eIF-2 X RF and almost the entire Mr 38,000 polypeptide component in RF remain unphosphorylated after prolonged incubation with HRI and ATP. A possible role of this free Mr 38,000 polypeptide in RF action is discussed.

L6 ANSWER 2 OF 3 CA COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 95:37331 CA
TITLE: Protein synthesis in rabbit reticulocytes. Purification and characterization of a double-stranded RNA-dependent protein synthesis inhibitor from reticulocyte lysates
AUTHOR(S): Das, Hriday K.; Das, Anathbandhu; Ghosh-Dastidar, Pradip; Ralston, Robert O.; Yaghmai, Bahram; Roy,

Reena; Gupta, Naba K.
CORPORATE SOURCE: Dep. Chem., Univ. Nebraska, Lincoln, NE, 68588, USA
SOURCE: Journal of Biological Chemistry (1981), 256(12), 6491-5
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Reticulocyte lysates contain a latent form of eukaryotic peptide chain initiation factor 2 (eIF-2) kinase (dsI) which becomes activated in the presence of double-stranded RNA and ATP and inhibits protein synthesis. The latent form of dsI was partially purified from reticulocyte ribosomal salt wash. The purified dsI was activated by incubation in the presence of poly(I).cntdot.poly(C) and [.gamma.32P]ATP and the activated dsI was further purified to near homogeneity. On SDS-polyacrylamide gel electrophoresis, purified [32P]dsI shows an intensely staining 67,000-dalton polypeptide band which corresponds to a single 67,000-dalton radioactive band. During Sephadex (G-200) gel filtration, both the latent form of dsI and the activated dsI elute similarly with a peak corresponding to a mol. wt. of 67,000. Purified dsI phosphorylates the 38,000-dalton subunit of eIF-2 and, under conditions of eIF-2 phosphorylation, dsI strongly inhibits AUG-dependent methionyl-tRNAf binding to 40 S ribosomes. Also, in partial reactions, eIF-2.alpha.(P) formed by phosphorylation of eIF-2 using dsI and ATP, is not recognized by two eIF-2 ancillary factors, Co-eIF-2B and Co-eIF-2C. Thus, like the heme-regulated eIF-2 kinase, dsI phosphorylates eIF-2 and eIF-2.alpha.(P) thus formed, and in both cases, is not recognized by Co-eIF-2B and Co-eIF-2C, and is inactive in some step(s) of methionyl-tRNAf.cntdot.40 S initiation complex formation.

L6 ANSWER 3 OF 3 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 80182264 MEDLINE
DOCUMENT NUMBER: 80182264 PubMed ID: 7372648
TITLE: Protein synthesis in rabbit reticulocytes. A study of the mechanism of interreaction of fluorescently labeled co-eIF-2A with eIF-2 using fluorescence polarization.
AUTHOR: Ghosh-Dastidar P; Giblin D; Yaghmai B; Das A; Das H K; Parkhurst L J; Gupta N K
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1980 May 10) 255 (9) 3826-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198007
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 20000303
Entered Medline: 19800722

AB 5-Dimethylaminonaphthalene-1-sulfonyl (dansyl)-Co-eIF-2A was prepared using homogeneous Co-eIF-2A. Dansyl-Co-eIF-2A was as active as untreated Co-eIF-2A when assayed for stimulation of ternary complex formation and also for protection of the ternary complex from dissociation by aurintricarboxylic acid. The mechanism of interaction of dansyl-Co-eIF-2A with eIF-2 was studied by measuring changes in fluorescence polarization. These studies indicate that dansyl-Co-eIF-2A interacts specifically with the ternary complex and does not interact with free eIF-2 or with two other high molecular weight protein complexes, Co-eIF-2B and Co-eIF-2C. Mg2+ inhibits ternary complex formation by eIF-2 and **Co-eIF-2C** relieves this Mg2+ **inhibition** of ternary complex formation. In both cases, the changes in fluorescence polarization of dansyl-Co-eIF-2A correlate well with the extent of ternary complex formed.

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=> d his

     (FILE 'HOME' ENTERED AT 12:31:12 ON 16 AUG 2003)

     FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 12:31:17 ON 16
     AUG 2003
L1          107 S (EUKARYOT? (N) TRANSLATION? (N) FACTOR (N) 2C?) OR (CO (N) EI
L2       130563 S ANTISENSE OR RNAI OR (ANTI (N) SENSE) OR (COMPLEMENT? (2N) (O
L3           16 S L1 AND L2
L4            6 DUP REM L3 (10 DUPLICATES REMOVED)
L5            8 S L1 (3N) INHIB?
L6            3 DUP REM L5 (5 DUPLICATES REMOVED)

=> dup rem l1
PROCESSING COMPLETED FOR L1
L7           42 DUP REM L1 (65 DUPLICATES REMOVED)

=> d l7 1-42 ibib abs

L7   ANSWER 1 OF 42     MEDLINE on STN                    DUPLICATE 1
ACCESSION NUMBER:   2003245107     MEDLINE
DOCUMENT NUMBER:    22652771   PubMed ID: 12767979
TITLE:              Structural basis for distinctions between substrate and
                    inhibitor specificities for feline immunodeficiency virus
                    and human immunodeficiency virus proteases.
AUTHOR:             Lin Ying-Chuan; Beck Zachary; Morris Garrett M; Olson
                    Arthur J; Elder John H
CORPORATE SOURCE:   Department of Molecular Biology, The Scripps Research
                    Institute, La Jolla, California 92037, USA.
CONTRACT NUMBER:    P01 GM48870 (NIGMS)
     R01 AI40882 (NIAID)
SOURCE:             JOURNAL OF VIROLOGY, (2003 Jun) 77 (12) 6589-600.
                    Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY:       United States
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200307
ENTRY DATE:         Entered STN: 20030528
                    Last Updated on STN: 20030704
                    Entered Medline: 20030703
AB   We used feline immunodeficiency virus (FIV) protease (PR) as a mutational
     framework to define determinants for the observed substrate and inhibitor
     specificity distinctions between FIV and human immunodeficiency virus
     (HIV) PRs. Multiple-substitution mutants were constructed by replacing
     the residues in and around the active site of FIV PR with the structurally
     equivalent residues of HIV-1 PR. Mutants included combinations of three
     critical regions (FIV numbering, with equivalent HIV numbering in
     superscript): I37(32)V in the active core region; N55(46)M, M56(47)I, and
     V59(50)I in the flap region; and L97(80)T, I98(81)P, Q99(82)V,
     P100(83)N, and L101(84)I in the 90s loop region. Significant alterations
     in specificity were observed, consistent with the involvement of these
     residues in determining the substrate-inhibitor specificity distinctions
     between FIV and HIV PRs. Two previously identified residues, I35 and I57
     of FIV PR, were intolerant to substitution and yielded inactive PRs.
     Therefore, we attempted to recover the activity by introducing secondary
     mutations. The addition of G62(53)F and K63(54)I, located at the top of
     the flap and outside the active site, compensated for the activity lost in
     the I57(48)G substitution mutants. An additional two substitutions,
     D105(88)N and N88(74)T, facilitated recovery of activity in mutants that
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included the I35(30)D substitution. Determination of K(i) values of potent HIV-1 PR inhibitors against these mutants showed that inhibitor specificity paralleled that of HIV-1 PR. The findings indicate that maintenance of both substrate and inhibitor specificity is a function of interactions between residues both inside and outside the active site. Thus, mutations apparently peripheral to the active site can have a dramatic influence on inhibitor efficacy.

L7 ANSWER 2 OF 42 MEDLINE on STN
ACCESSION NUMBER: 2003372527 IN-PROCESS
DOCUMENT NUMBER: 22788786 PubMed ID: 12906857
TITLE: Identification of eight members of the Argonaute family in the human genome small star, filled.
AUTHOR: Sasaki Takashi; Shiohama Aiko; Minoshima Shinsei; Shimizu Nobuyoshi
CORPORATE SOURCE: Department of Molecular Biology, Keio University School of Medicine, 35 Shinanomachi, Shinjuku-ku, 160-8582, Tokyo, Japan.
SOURCE: GENOMICS, (2003 Sep) 82 (3) 323-30.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20030809
Last Updated on STN: 20030809

AB A number of genes have been identified as members of the Argonaute family in various nonhuman organisms and these genes are considered to play important roles in the development and maintenance of germ-line stem cells. In this study, we identified the human Argonaute family, consisting of eight members. Proteins to be produced from these family members retain a common architecture with the PAZ motif in the middle and Piwi motif in the C-terminal region. Based on the sequence comparison, eight members of the Argonaute family were classified into two subfamilies: the PIWI subfamily (PIWIL1/HIWI, PIWIL2/HILI, PIWIL3, and PIWIL4/HIWI2) and the **eIF2C**/AGO subfamily (EIF2C1/hAGO1, EIF2C2/hAGO2, EIF2C3/hAGO3, and EIF2C4/hAGO4). PCR analysis using human multitissue cDNA panels indicated that all four members of the PIWI subfamily are expressed mainly in the testis, whereas all four members of the **eIF2C**/AGO subfamily are expressed in a variety of adult tissues. Immunoprecipitation and affinity binding experiments using human HEK293 cells cotransfected with cDNAs for FLAG-tagged DICER, a member of the ribonuclease III family, and the His-tagged members of the Argonaute family suggested that the proteins from members of both subfamilies are associated with DICER. We postulate that at least some members of the human Argonaute family may be involved in the development and maintenance of stem cells through the RNA-mediated gene-quelling mechanisms associated with DICER.

L7 ANSWER 3 OF 42 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2003020539 IN-PROCESS
DOCUMENT NUMBER: 22414943 PubMed ID: 12526743
TITLE: Short-interfering-RNA-mediated gene silencing in mammalian cells requires Dicer and **eIF2C** translation initiation factors.
AUTHOR: Doi Noboru; Zenno Shuhei; Ueda Ryu; Ohki-Hamazaki Hiroko; Ui-Tei Kumiko; Saigo Kaoru
CORPORATE SOURCE: Department of Biophysics, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, 113-0033, Bunkyo-ku, Tokyo, Japan.
SOURCE: CURRENT BIOLOGY, (2003 Jan 8) 13 (1) 41-6.
Journal code: 9107782. ISSN: 0960-9822.

PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
OTHER SOURCE: GDB-AB028449; GENBANK-AB046787; GENBANK-AB081470; GENBANK-AB081471; GENBANK-AB081472; GENBANK-AB081473; GENBANK-AB081474
ENTRY DATE: Entered STN: 20030116
Last Updated on STN: 20030715

AB RNA interference (RNAi) is the process of long, double-stranded (ds), RNA-dependent posttranscriptional gene silencing (PTGS). In lower eukaryotes, dsRNA introduced into the cytoplasm is cleaved by the RNaseIII-like enzyme, Dicer, to 21-23 nt RNA (short interfering [si] RNA), which may serve as guide for target mRNA degradation. In mammals, long-dsRNA-dependent PTGS is applicable only to a limited number of cell types, whereas siRNA synthesized in vitro is capable of effectively inducing gene silencing in a wide variety of cells. Although biochemical and genetic analyses in lower eukaryotes showed that Dicer and some PIWI family member proteins are essential for long-dsRNA-dependent PTGS, little is known about the molecular mechanisms underlying siRNA-based PTGS. Here, we show that Dicer and **eIF2C** translation initiation factors belonging to the PIWI family (eIF2C1-4) play an essential role in mammalian siRNA-mediated PTGS, most probably through synergistic interactions. Immunoprecipitation experiments suggest that, in human and mouse cells, complex formation occurs between Dicer and eIF2C1 or 2 and that the PIWI domain of **eIF2C** is essential for the formation of this complex.

L7 ANSWER 4 OF 42 CA COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 139:80222 CA
TITLE: Protein and cDNA sequences of 21.56-kilodalton human initiation factor **eIF2C**-like protein and their therapeutic uses
INVENTOR(S): Mao, Yumin; Xie, Yi
PATENT ASSIGNEE(S): Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 32 pp. CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| CN 1363568 | A | 20020814 | CN 2001-105038 | 20010105 |

PRIORITY APPLN. INFO.: CN 2001-105038 20010105

AB The invention provides protein and cDNA sequences of a novel 21.56-kilodalton human protein, designated as "initiation factor **eIF2C** 21.56", which has similar expression pattern to that of known initiation factor **eIF2C**. The invention relates to expression of initiation factor **eIF2C**-like protein in E. coli BL21(DE3)plySs transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against initiation factor **eIF2C** -like protein. The invention further relates to the uses of the initiation factor **eIF2C**-like protein in treatment of initiation factor **eIF2C**-related diseases (such as neoplasm, blood disease, HIV infection, immune disease, inflammation, etc).

L7 ANSWER 5 OF 42 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 2002470265 MEDLINE
DOCUMENT NUMBER: 22217361 PubMed ID: 12230974

TITLE: Single-stranded antisense siRNAs guide target RNA cleavage in RNAi.
AUTHOR: Martinez Javier; Patkaniowska Agnieszka; Urlaub Henning; Luhrmann Reinhard; Tuschl Thomas
CORPORATE SOURCE: Department of Cellular Biochemistry, Max-Planck-Institute for Biophysical Chemistry, Am Fassberg 11, D-37077, Gottingen, Germany.
SOURCE: CELL, (2002 Sep 6) 110 (5) 563-74.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200302
ENTRY DATE: Entered STN: 20020917
Last Updated on STN: 20030207
Entered Medline: 20030206

AB Small interfering RNAs (siRNAs) are the mediators of mRNA degradation in the process of RNA interference (RNAi). Here, we describe a human biochemical system that recapitulates siRNA-mediated target RNA degradation. By using affinity-tagged siRNAs, we demonstrate that a single-stranded siRNA resides in the RNA-induced silencing complex (RISC) together with eIF2C1 and/or eIF2C2 (human **GERp95**) Argonaute proteins. RISC is rapidly formed in HeLa cell cytoplasmic extract supplemented with 21 nt siRNA duplexes, but also by adding single-stranded antisense RNAs, which range in size between 19 and 29 nucleotides. Single-stranded antisense siRNAs are also effectively silencing genes in HeLa cells, especially when 5'-phosphorylated, and expand the repertoire of RNA reagents suitable for gene targeting.

L7 ANSWER 6 OF 42 CA COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 134:336728 CA
TITLE: Protein and cDNA sequences of a novel human protein formation initiation factor 28 and diagnostic and therapeutic uses thereof
INVENTOR(S): Mao, Yumin; Xie, Yi
PATENT ASSIGNEE(S): Shanghai Bio Road Gene Development Ltd., Peop. Rep. China
SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2001031001 | A1 | 20010503 | WO 2000-CN382 | 20001027 |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| CN 1302874 | A | 20010711 | CN 1999-119888 | 19991028 |

PRIORITY APPLN. INFO.: CN 1999-119888 A 19991028

AB The invention provides protein and cDNA sequences for a novel human protein formation initiation factor 28, which shares sequence homol. with rabbit protein formation initiation factor **eIF2C**. The invention

also relates to constructs and methods to express the cloned gene for the prepn. of its protein and antibodies using E.coli cells or eukaryotic cells, and diagnostic and therapeutic uses for protein formation initiation factor 28 related diseases.
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 42 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2001652579 MEDLINE
DOCUMENT NUMBER: 21560960 PubMed ID: 11553639
TITLE: **GERp95** belongs to a family of signal-transducing proteins and requires Hsp90 activity for stability and Golgi localization.
AUTHOR: Tahbaz N; Carmichael J B; Hobman T C
CORPORATE SOURCE: Department of Cell Biology, University of Alberta, Edmonton T6G 2H7, Canada.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Nov 16) 276 (46) 43294-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011114
Last Updated on STN: 20030105
Entered Medline: 20011226

AB **GERp95** (Golgi-endoplasmic reticulum protein 95 kDa) is part of a large family of highly conserved proteins found in all metazoans and the fission yeast Schizosaccharomyces pombe. Genetic studies suggest that homologs of **GERp95** are components of signaling pathways that regulate cellular differentiation, development, and RNA interference. However, the precise molecular functions of these proteins remain unknown. Genetic analysis of **GERp95** homologs has been complicated by the presence of multiple genes with overlapping functions in most organisms. Binding partners for members of this protein family have not been identified. The purpose of this study was to identify proteins that associate with **GERp95**. Glutathione S-transferase-**GERp95** fusions were expressed in transfected cells, and proteins that bound to **GERp95** were co-purified using glutathione-agarose beads. The amino-terminal region of **GERp95** was found to interact with the specialized chaperone Hsp90 and a number of its cognate binding proteins. Inhibition of Hsp90 activity with geldanamycin or radicicol resulted in rapid degradation of newly synthesized **GERp95**. The membrane-associated pool of **GERp95** was not bound to Hsp90, although activity of this chaperone was required for stable association of **GERp95** with the Golgi in normal rat kidney cells. These results indicate that **GERp95** engages an Hsp90 chaperone complex prior to association with intracellular membranes.

L7 ANSWER 8 OF 42 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 2001481517 MEDLINE
DOCUMENT NUMBER: 21417217 PubMed ID: 11526087
TITLE: Aubergine encodes a Drosophila polar granule component required for pole cell formation and related to **eIF2C**.
AUTHOR: Harris A N; Macdonald P M
CORPORATE SOURCE: Department of Biological Sciences, Stanford University, Stanford, CA 94305, USA.
CONTRACT NUMBER: GM54409 (NIGMS)
SOURCE: DEVELOPMENT, (2001 Jul) 128 (14) 2823-32.
Journal code: 8701744. ISSN: 0950-1991.

PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF334408; GENBANK-AF334409; GENBANK-AF334410; GENBANK-AF334411; GENBANK-AF334412
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010830
Last Updated on STN: 20020907
Entered Medline: 20011011

AB In Drosophila oocytes, activation of Oskar translation from a transcript localized to the posterior pole is an essential step in the organization of the pole plasm, specialized cytoplasm that contains germline and abdominal body patterning determinants. Oskar is a component of polar granules, large particles associated with the pole plasm and the germline precursor pole cells of the embryo. aubergine mutants fail to translate oskar mRNA efficiently and are thus defective in posterior body patterning and pole cell formation. We have found that Aubergine protein is related to eukaryotic translation initiation factor 2C and suggest how it may activate translation. In addition, we found that Aubergine was recruited to the posterior pole in a vas-dependent manner and is itself a polar granule component. Consistent with its presence in these structures, Aubergine is required for pole cell formation independently of its initial role in oskar translation. Unlike two other known polar granule components, Vasa and Oskar, Aubergine remains cytoplasmic after pole cell formation, suggesting that the roles of these proteins diverge during embryogenesis.

L7 ANSWER 9 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
ACCESSION NUMBER: 2001:537161 BIOSIS
DOCUMENT NUMBER: PREV200100537161
TITLE: A methodology for analysis of sugarcane productivity trends. I. Analysis across districts.
AUTHOR(S): Ellis, R. N.; Basford, K. E. (1); Cooper, M.; Leslie, J. K.; Byth, D. E.
CORPORATE SOURCE: (1) School of Land and Food Sciences, The University of Queensland, Brisbane, Qld, 4072 Australia
SOURCE: Australian Journal of Agricultural Research, (2001) Vol. 52, No. 10, pp. 1001-1009. print.
ISSN: 0004-9409.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Historically, few articles have addressed the use of district level mill production data for analysing the effect of varietal change on sugarcane productivity trends. This appears to be due to lack of compiled district data sets and appropriate methods by which to analyse these data. Recently, varietal data on tonnes of sugarcane per hectare (TCH), sugar content (CCS), and their product, tonnes of sugar content per hectare (TSH) on a district basis, have been compiled. This study was conducted to develop a methodology for regular analysis of such data from mill districts to assess productivity trends over time, accounting for variety and variety X environment interaction effects for 3 mill districts (Mulgrave, Babinda, and Tully) from 1958 to 1995. Restricted maximum likelihood methodology was used to analyse the district level data and best linear unbiased predictors for random effects, and best linear unbiased estimates for fixed effects were computed in a mixed model analysis. In the combined analysis over districts, Q124 was the top ranking variety for TCH, and Q120 was top ranking for both CCS and TSH. Overall production for TCH increased over the 38-year period investigated. Some of this increase can be attributed to varietal improvement, although

the predictors for TCH have shown little progress since the introduction of **Q99** in 1976. Although smaller gains have been made in varietal improvement for CCS, overall production for CCS decreased over the 38 years due to non-varietal factors. Varietal improvement in TSH appears to have peaked in the mid-1980s. Overall production for TSH remained stable over time due to the varietal increase in TCH and the non-varietal decrease in CCS.

L7 ANSWER 10 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7
ACCESSION NUMBER: 2001:557226 BIOSIS
DOCUMENT NUMBER: PREV200100557226
TITLE: PTGS in plants, a virus resistance mechanism. Original Title: L'inactivation epigenetique post-transcriptionnelle chez les vegetaux: Un mecanisme de resistance aux virus..
AUTHOR(S): Beclin, Christophe (1); Vaucheret, Herve
CORPORATE SOURCE: (1) Laboratoire de Biologie Cellulaire, UR 501, INRA, 78026, Versailles Cedex: beclin@versailles.inra.fr, vauchere@versailles.inra.fr France
SOURCE: M-S (Medecine Sciences), (Septembre, 2001) Vol. 17, No. 8-9, pp. 845-855. print.
ISSN: 0767-0974.
DOCUMENT TYPE: General Review
LANGUAGE: French
SUMMARY LANGUAGE: English; French
AB Post-transcriptional gene silencing (PTGS) in plants and quelling in fungi are transgene-induced silencing phenomena, resulting from the degradation of transgene RNAs and homologous endogenous RNAs. PTGS shows similarities with RNAi in animals, a phenomenon induced by injection of double-stranded RNA (dsRNA) or introduction of transgenes expressing dsRNA. First, PTGS and RNAi both involve dsRNA. Second, they can be dissected into three steps: localized initiation, propagation of a sequence-specific systemic signal, maintenance in silenced tissues. Finally, they both correlate with the accumulation of 25nt sense and anti-sense RNAs. Genetic dissection and cloning of genes regulating PTGS, quelling and RNAi confirmed the links between these three phenomena. Indeed, all three involve a putative RNA-dependent-RNA polymerase and a protein similar to the translation initiator factor **eIF2C**. However some differences can be noticed. In particular, PTGS in plants requires two genes, SGS3 (encoding a protein of unknown function) and MET1 (encoding a DNA-methyltransferase), which are not required for RNAi. Indeed, the genomes of C. elegans and Drosophila (two organisms undergoing RNAi) lack both methylation and orthologs of the SGS3 gene). Several experiments revealed that PTGS is a general mechanism of virus resistance. In particular, we showed that Arabidopsis mutants impaired in PTGS are hypersensitive to infection by the virus CMV. However, many viruses have developed strategies to counteract PTGS and therefore succeed to infect plants. Because viruses may act as targets, inducers or inhibitors of PTGS, the success and the extent of virus infection therefore depends on the competition between plant PTGS defenses and virus counteracting effects.

L7 ANSWER 11 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8
ACCESSION NUMBER: 2002:165396 BIOSIS
DOCUMENT NUMBER: PREV200200165396
TITLE: **GERp95** belongs to a family of proteins involved in novel signaling pathways and requires Hsp90 activity for stability and Golgi localization.
AUTHOR(S): Tahbaz, Nasser (1); Carmichael, Jon B. (1); Hobman, Tom C. (1)
CORPORATE SOURCE: (1) Cell Biology, University of Alberta, 5-51, Medical

Science Building, Edmonton, AB, T6G 2H7 Canada
SOURCE: Molecular Biology of the Cell, (Nov, 2001) Vol. 12, No. Supplement, pp. 238a-239a. http://www.molbiolcell.org/. print.
Meeting Info.: 41st Annual Meeting of the American Society for Cell Biology Washington DC, USA December 08-12, 2001
ISSN: 1059-1524.
DOCUMENT TYPE: Conference
LANGUAGE: English

L7 ANSWER 12 OF 42 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 2001:812443 SCISEARCH
THE GENUINE ARTICLE: 479TM
TITLE: Two mouse piwi-related genes: miwi and mili
AUTHOR: Kuramochi-Miyagawa S; Kimura T; Yomogida K; Kuroiwa A; Tadokoro Y; Fujita Y; Sato M; Matsuda Y; Nakano T (Reprint)
CORPORATE SOURCE: Osaka Univ, Microbial Dis Res Inst, Dept Mol Cell Biol, 3-1 Yamada Oka, Suita, Osaka 5650871, Japan (Reprint); Osaka Univ, Microbial Dis Res Inst, Dept Mol Cell Biol, Suita, Osaka 5650871, Japan; Osaka Univ, Microbial Dis Res Inst, Dept Sci Lab Anim Experimentat, Suita, Osaka 5650871, Japan; Hokkaido Univ, Div Biosci, Grad Sch Environm Earth Sci, Lab Cytogenet, Kita Ku, Sapporo, Hokkaido 0600810, Japan; Hokkaido Univ, Fac Sci, Chromosome Res Unit, Kita Ku, Sapporo, Hokkaido 0600810, Japan
COUNTRY OF AUTHOR: Japan
SOURCE: MECHANISMS OF DEVELOPMENT, (OCT 2001) Vol. 108, No. 1-2, pp. 121-133.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0925-4773.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 30
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB Genes belonging to the piwi family are required for stem cell self-renewal in diverse organisms. We cloned mouse homologues of piwi by RT-PCR using degenerative primers. The deduced amino acid sequences of mouse homologues MIWI and MILI showed that each contains a well-conserved C-terminal PIWI domain and that each shares significant homology with PIWI and their human counterparts HIWI. Both miwi and mili were found in germ cells of adult testis by in situ hybridization, suggesting that these genes may function in spermatogenesis. Furthermore, mili was expressed in primordial germ cells (PGCs) of developing mouse embryos and may therefore play a role during germ cell formation. MIWI may be involved in RNA processing or translational regulation, since MIWI was found to possess RNA binding activity. Our data suggest that miwi and mili regulate spermatogenesis and primordial germ cell production. (C) 2001 Elsevier Science Ireland Ltd. All rights reserved.

L7 ANSWER 13 OF 42 CA COPYRIGHT 2003 ACS on STN DUPLICATE 9
ACCESSION NUMBER: 135:243915 CA
TITLE: The use of orthogonal signal correction to improve NIR readings of pulp fiber properties
AUTHOR(S): Champagne, M.; Meglen, B.; Wold, S.; Kettaneh-Wold, N.
CORPORATE SOURCE: Can.
SOURCE: Pulp & Paper Canada (2001), 102(4), 41-43
CODEN: PPCAAA; ISSN: 0316-4004
PUBLISHER: Southam Inc.
DOCUMENT TYPE: Journal

LANGUAGE: English

AB In 1999, a methodol. was developed to use Near-IR (NIR) Technol. of inhouse pulp fiber quality properties **Q99** and Q97. The initial results with dry samples of pulp were encouraging. The wet samples results were initially disappointing using the std. chemometric techniques. A new chemometric method was developed, called Orthogonal Signal Correction (OSC), which was used to obtain a good correction of **Q99** in the wet pulp samples.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 42 CA COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 134:209505 CA

TITLE: The use of OSC and wavelets to improve NIR readings of pulp properties

AUTHOR(S): Champagne, M.; Meglen, B.; Wold, S.; Kettaneh-Wold, N.

CORPORATE SOURCE: Tembec Industries Inc., Temiscaming, QC, Can.

SOURCE: Preprint - Control Systems 2000: Quantifying the Benefits of Process Control, Victoria, BC, Canada, May 1-4, 2000 (2000), 271-274. Pulp and Paper Technical Association of Canada: Montreal, Que.
CODEN: 69AHBP

DOCUMENT TYPE: Conference

LANGUAGE: English

AB In 1999, Tembec Industries and the National Renewal Energy Labs. worked together in developing a methodol. to use Near-IR (NIR) Technol. of pulp properties **Q99** and Q97. The initial results with dry samples of pulp were encouraging. However, the wet samples results were initially disappointing, using the std. chemometric techniques. A new chemometric method, called Orthogonal Signal Correction (OSC) was developed and used to obtain a good correction of **Q99** in the wet pulp samples.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 42 CA COPYRIGHT 2003 ACS on STN DUPLICATE 10

ACCESSION NUMBER: 133:262069 CA

TITLE: Kazakh strains of tobacco mosaic virus: two strains with potentially destabilizing amino acid substitutions in the coat protein

AUTHOR(S): Novikov, Victor K.; Belenovich, Ekaterina V.; Dobrov, Evgeny N.; Zavriev, Sergei K.

CORPORATE SOURCE: Department of Virology and Belozersky Institute of Physico-Chemical Biology, Moscow State University, Moscow, 119899, Russia

SOURCE: Physiological and Molecular Plant Pathology (2000), 56(2), 71-77
CODEN: PMPPEZ; ISSN: 0885-5765

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Some properties of two Kazakh strains (K1 and K2) of tobacco mosaic virus (TMV) are described. K1 had been isolated by Dr M. Gol'din in 1963, and K2 recently in our lab. Both strains were rather similar in host range and antigenic properties to the tomato strain of TMV (tomato mosaic virus, ToMV), but differed from the latter by inducing unusual symptoms on upper non-inoculated leaves of infected tobacco plants. K1 was semi-defective and temp.-sensitive, and formed large amts. of long RNA-free helical protein rods in infected plants. K2 was found to be neither defective nor temp.-sensitive, and did not produce protein rods in infected cells. K1 and K2 coat protein gene sequencing data showed, as expected, that both proteins are similar in primary structure to ToMV coat protein: only three amino acid substitutions, relative to ToMV, were found in K1 and five in

K2 coat protein. Two of these substitutions are unusual, namely, substitution of normally strictly conserved R92 by S (with concomitant Q99 R change) in K2 and substitution of K53 by E in K1. (c) 2000 Academic Press.
REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 16 OF 42 MEDLINE on STN DUPLICATE 11
ACCESSION NUMBER: 1999443791 MEDLINE
DOCUMENT NUMBER: 99443791 PubMed ID: 10512872
TITLE: **GERp95**, a membrane-associated protein that belongs to a family of proteins involved in stem cell differentiation.
AUTHOR: Cikaluk D E; Tahbaz N; Hendricks L C; DiMattia G E; Hansen D; Pilgrim D; Hobman T C
CORPORATE SOURCE: Department of Cell Biology, University of Alberta, Edmonton, AB, T6G 2H7, Canada.
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (1999 Oct) 10 (10) 3357-72. Journal code: 9201390. ISSN: 1059-1524.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF195534
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991202
AB A panel of mAbs was elicited against intracellular membrane fractions from rat pancreas. One of the antibodies reacted with a 95-kDa protein that localizes primarily to the Golgi complex or the endoplasmic reticulum (ER), depending on cell type. The corresponding cDNA was cloned and sequenced and found to encode a protein of 97.6 kDa that we call **GERp95 (Golgi ER protein 95 kDa)**. The protein copurifies with intracellular membranes but does not contain hydrophobic regions that could function as signal peptides or transmembrane domains. Biochemical analysis suggests that **GERp95** is a cytoplasmically exposed peripheral membrane protein that exists in a protease-resistant complex. **GERp95** belongs to a family of highly conserved proteins in metazoans and Schizosaccharomyces pombe. It has recently been determined that plant and Drosophila homologues of **GERp95** are important for controlling the differentiation of stem cells (Bohmert et al., 1998; Cox et al., 1998; Moussian et al., 1998). In Caenorhabditis elegans, there are at least 20 members of this protein family. To this end, we have used RNA interference to show that the **GERp95** orthologue in C. elegans is important for maturation of germ-line stem cells in the gonad. **GERp95** and related proteins are an emerging new family of proteins that have important roles in metazoan development. The present study suggests that these proteins may exert their effects on cell differentiation from the level of intracellular membranes.

L7 ANSWER 17 OF 42 MEDLINE on STN DUPLICATE 12
ACCESSION NUMBER: 1999094873 MEDLINE
DOCUMENT NUMBER: 99094873 PubMed ID: 9876176
TITLE: The PINHEAD/ZWILLE gene acts pleiotropically in Arabidopsis development and has overlapping functions with the ARGONAUTE1 gene.
AUTHOR: Lynn K; Fernandez A; Aida M; Sedbrook J; Tasaka M; Masson P; Barton M K
CORPORATE SOURCE: Program in Cellular and Molecular Biology and Department of Genetics, University of Wisconsin-Madison, Madison, WI

53706, USA.. mkbarton@facstaff.wisc.edu
SOURCE: DEVELOPMENT, (1999 Feb) 126 (3) 469-81.
Journal code: 8701744. ISSN: 0950-1991.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-AF154272
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 20011025
Entered Medline: 19990304

AB Several lines of evidence indicate that the adaxial leaf domain possesses a unique competence to form shoot apical meristems. Factors required for this competence are expected to cause a defect in shoot apical meristem formation when inactivated and to be expressed or active preferentially in the adaxial leaf domain. PINHEAD, a member of a family of proteins that includes the translation factor **eIF2C**, is required for reliable formation of primary and axillary shoot apical meristems. In addition to high-level expression in the vasculature, we find that low-level PINHEAD expression defines a novel domain of positional identity in the plant. This domain consists of adaxial leaf primordia and the meristem. These findings suggest that the PINHEAD gene product may be a component of a hypothetical meristem forming competence factor. We also describe defects in floral organ number and shape, as well as aberrant embryo and ovule development associated with pinhead mutants, thus elaborating on the role of PINHEAD in Arabidopsis development. In addition, we find that embryos doubly mutant for PINHEAD and ARGONAUTE1, a related, ubiquitously expressed family member, fail to progress to bilateral symmetry and do not accumulate the SHOOT MERISTEMLESS protein. Therefore PINHEAD and ARGONAUTE1 together act to allow wild-type growth and gene expression patterns during embryogenesis.

L7 ANSWER 18 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1999:531676 BIOSIS
DOCUMENT NUMBER: PREV199900531676
TITLE: Anti-Su autoantibodies recognize the human homologue of rabbit initiation factor **eIF2C**.
AUTHOR(S): Takeda, Yoshihiko (1); Dynan, William S. (1); Hardin, John A. (1)
CORPORATE SOURCE: (1) Augusta, GA USA
SOURCE: Arthritis & Rheumatism, (Sept., 1999) Vol. 42, No. 9 SUPPL., pp. S384.
Meeting Info.: 63rd Annual Scientific Meeting of the American College of Rheumatology and the 34th Annual Scientific Meeting of the Association of Rheumatology Health Professionals Boston, Massachusetts, USA November 13-17, 1999
ISSN: 0004-3591.
DOCUMENT TYPE: Conference
LANGUAGE: English

L7 ANSWER 19 OF 42 MEDLINE on STN DUPLICATE 13
ACCESSION NUMBER: 2000005943 MEDLINE
DOCUMENT NUMBER: 20005943 PubMed ID: 10534406
TITLE: Human eukaryotic initiation factor EIF2C1 gene: cDNA sequence, genomic organization, localization to chromosomal bands 1p34-p35, and expression.
AUTHOR: Koesters R; Adams V; Betts D; Moos R; Schmid M; Siermann A; Hassam S; Weitz S; Lichter P; Heitz P U; von Knebel Doeberitz M; Briner J
CORPORATE SOURCE: Institute of Clinical Pathology, Department of Pathology,

University Hospital of Zurich, Schmelzbergstrasse 12, Zurich, 8091, Switzerland.. R.Koesters@dkfz-heidelberg.de
SOURCE: GENOMICS, (1999 Oct 15) 61 (2) 210-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF093097; GENBANK-AF121255
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991209

AB We report the cloning and characterization of the human eukaryotic protein translation initiation factor EIF2C1 gene. The human EIF2C1 gene consists of 19 exons and 18 introns that span a region of almost 50 kb. It is located on the short arm of chromosome 1 in the region 1p34-p35. This genomic region is frequently lost in human cancers such as Wilms tumors, neuroblastoma, and carcinomas of the breast, liver, and colon. The human EIF2C1 gene is ubiquitously expressed at low to medium levels. Differential polyadenylation and splicing result in a complex transcriptional pattern. The cDNA sequence is 7478 bp long and contains an extremely large 3' untranslated region of 4799 bp with multiple, short repeated segments composed of mono-, tri-, or quattronucleotides interspersed throughout. The human EIF2C1 gene belongs to a multigene family in human. It is highly conserved during evolution, sharing about 90% identity with rabbit **eIF2C** and 70% identity with plant AGO1 at the amino acid level. These facts suggest that human EIF2C1 might play an important physiological role.


L7 ANSWER 20 OF 42 MEDLINE on STN DUPLICATE 14
ACCESSION NUMBER: 2000004389 MEDLINE
DOCUMENT NUMBER: 20004389 PubMed ID: 10535731
TITLE: The rde-1 gene, RNA interference, and transposon silencing in C. elegans.
AUTHOR: Tabara H; Sarkissian M; Kelly W G; Fleenor J; Grishok A; Timmons L; Fire A; Mello C C
CORPORATE SOURCE: Department of Cell Biology, Program in Molecular Medicine, University of Massachusetts Cancer Center, Worcester 01605, USA.
CONTRACT NUMBER: GM37706 (NIGMS)
GM58800 (NIGMS)
HD08353 (NICHD)
SOURCE: CELL, (1999 Oct 15) 99 (2) 123-32.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF180730
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991110

AB Double-stranded (ds) RNA can induce sequence-specific inhibition of gene function in several organisms. However, both the mechanism and the physiological role of the interference process remain mysterious. In order to study the interference process, we have selected C. elegans mutants resistant to dsRNA-mediated interference (RNAi). Two loci, rde-1 and rde-4, are defined by mutants strongly resistant to RNAi but with no obvious defects in growth or development. We show that rde-1 is a member

of the piwi/sting/argonaute/zwille/**eIF2C** gene family conserved from plants to vertebrates. Interestingly, several, but not all, RNAi-deficient strains exhibit mobilization of the endogenous transposons. We discuss implications for the mechanism of RNAi and the possibility that one natural function of RNAi is transposon silencing.

L7 ANSWER 21 OF 42 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 1998:906367 SCISEARCH
THE GENUINE ARTICLE: 137GQ
TITLE: Identification and characterization of **GERp95**, a novel membrane-associated protein
AUTHOR: Cikaluk D E (Reprint); Hendricks L C; Hanson D; Pilgrim D; Hobman T C
CORPORATE SOURCE: UNIV ALBERTA, EDMONTON, AB T6G 2M7, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (NOV 1998) Vol. 9, Supp. [S], pp. 455-455.
Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.
ISSN: 1059-1524.
DOCUMENT TYPE: Conference; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 0

L7 ANSWER 22 OF 42 MEDLINE on STN DUPLICATE 15
ACCESSION NUMBER: 1998267198 MEDLINE
DOCUMENT NUMBER: 98267198 PubMed ID: 9602122
TITLE: Molecular cloning and characterization of a rabbit **eIF2C** protein.
AUTHOR: Zou C; Zhang Z; Wu S; Osterman J C
CORPORATE SOURCE: Department of Chemistry, University of Nebraska, Lincoln, NE 68588, USA.
CONTRACT NUMBER: GM22079 (NIGMS)
SOURCE: GENE, (1998 May 12) 211 (2) 187-94.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF005355
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980723
Last Updated on STN: 20000303
Entered Medline: 19980714

AB Rabbit **eIF2C** (94kDa) has been shown to play important roles in the eukaryotic peptide chain initiation process. In this study, the primary structure of rabbit **eIF2C** is determined by cDNA cloning. Based on the partial amino acid sequences of Endolys C cleaved fragments, degenerate oligonucleotides were synthesized and used as primers for the polymerase chain reaction to amplify the corresponding cDNA fragment from a rabbit liver cDNA library. This fragment was subsequently used to screen for larger cDNAs. Marathon cDNA amplification and 5'-rapid amplification of cDNA ends were used to confirm the translation start site. Sequences from the overlapping clones were assembled into a 3599-bp composite sequence, which contains a single open reading frame that translates into a 813-deduced amino acid sequence. Northern blot analysis of rabbit liver ploy(A)+ RNA yielded a single message species at approximately 4.6kb. Western blot analysis of rabbit reticulocyte lysate using polyclonal antibody against the 94kDa **eIF2C** detected a higher-molecular-weight polypeptide (140kDa). No 94kDa polypeptide was detected. The cloned cDNA was further characterized by in-vitro

transcription-coupled translation in reticulocyte lysate. The translated product was precipitated with antibodies against **eIF2C**. Genomic Southern blot analysis indicates that the rabbit **eIF2C** is a single copy gene. Sequence analysis reveals that rabbit **eIF2C** has strong homology with a hypothetical protein in Caenorhabditis elegans.

L7 ANSWER 23 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1999:15637 BIOSIS
DOCUMENT NUMBER: PREV199900015637
TITLE: Identification and characterization of **GERp95**, a novel membrane-associated protein.
AUTHOR(S): Cikaluk, Darren E.; Hendricks, Linda C.; Hanson, Dave; Pilgrim, Dave; Hobman, Torn C.
CORPORATE SOURCE: Univ. Alberta, Alberta, MB Canada
SOURCE: Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No. SUPPL., pp. 79A.
Meeting Info.: 38th Annual Meeting of the American Society for Cell Biology San Francisco, California, USA December 12-16, 1998 American Society for Cell Biology
. ISSN: 1059-1524.
DOCUMENT TYPE: Conference
LANGUAGE: English

L7 ANSWER 24 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 16
ACCESSION NUMBER: 1996:536175 BIOSIS
DOCUMENT NUMBER: PREV199699258531
TITLE: Control of Caribbean fruit fly (Diptera: Tephritidae) in navel orange by forced hot air.
AUTHOR(S): Sharp, Jennifer L.; McGuire, Raymond G.
CORPORATE SOURCE: Subtrop. Hortic. Res. Stn., USDA-ARS, 13601 Old Cutler Rd., Miami, FL 33158 USA
SOURCE: Journal of Economic Entomology, (1996) Vol. 89, No. 5, pp. 1181-1185.
ISSN: 0022-0493.
DOCUMENT TYPE: Article
LANGUAGE: English
AB A single-stage, hot-air quarantine treatment was used to kill Caribbean fruit fly, Anastrepha suspensa (Loew), mature 3rd instars in Florida-grown 'Golden' navel orange, Citrus sinensis (L.) Osbeck. Treating infested navel orange with 48 +- 0.3 degree C forced air for 55.9 +- 0.3, 73.7 +- 1.3, and 119.4 +- 0.7 min, to reach final center pulp temperatures of 36-37, 40-41, and 44-45 degree C, respectively, when initial center pulp temperatures were 22.3 +- 0.2, 21.2 +- 0.2, and 20.5 +- 0.3 degree C, respectively, reduced the number of surviving puparia that developed from treated larvae. The exposure time needed to reach **Q99**.9968% mortality was 108.6 min (lower and upper fiducial limits were 88.4 and 200.3 min, respectively) when the final mean center pulp temperature was gtoreq 44 degree C. A large-scale confirmatory test resulted in no survivors when 113,676 Caribbean fruit fly larvae in 1,200 manually infested navel oranges were heated with 48 t 0.3 degree C forced air at an average 0.75 m-3/s air flow rate until the center pulp temperatures were gtoreq 44 degree C, which required 100.2 +- 3.0 min of heating when initial center pulp temperatures were 23.2 +- 0.4 degree C. Relative humidity ranged from 63.5% at the start of the test to 77.3% when the test was finished. After treatment at 48 +- 0.3 degree C for 105 min and 1 mo of storage at 5 degree C, there was no significant difference in quality characteristics between heated and unheated navel oranges.

L7 ANSWER 25 OF 42 MEDLINE on STN DUPLICATE 17
ACCESSION NUMBER: 95092776 MEDLINE
DOCUMENT NUMBER: 95092776 PubMed ID: 7999777

TITLE: Thermodynamic characterization of the cooperativity of 40S complex formation during the initiation of eukaryotic protein synthesis.
AUTHOR: Parkhurst K M; Hileman R E; Saha D; Gupta N K; Parkhurst L J
CORPORATE SOURCE: Department of Chemistry, University of Nebraska--Lincoln, 68588-0304.
CONTRACT NUMBER: DK 36288 (NIDDK)
GM 22079 (NIGMS)
SOURCE: BIOCHEMISTRY, (1994 Dec 20) 33 (50) 15168-77.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199501
ENTRY DATE: Entered STN: 19950215
Last Updated on STN: 20000303
Entered Medline: 19950124

AB The first step in mammalian protein synthesis is the formation of the 40S initiation complex, composed of the 40S ribosomal subunit (R), mRNA (M, here, a 10-mer oligoribonucleotide analogue containing the initiation codon), and the quaternary complex (Q, composed of eIF-2, GTP, Met-tRNA(fMet), and the ancillary protein factor **Co-eIF -2C**). The interdependence of the binding of R, M, and Q in forming the 40S complex is currently unclear. We have determined the thermodynamic parameters that characterize these interactions. The binary constants for R+M and Q+M were determined spectroscopically, measuring changes in the anisotropy of the fluorescence emission of 3'-fluorescein labeled M. The other binary constant, for Q+R, and the ternary constant were determined from Millipore filtration assays using radiolabeled Met-tRNA(fMet). The association constants for the binary reactions were as follows: Ka(Q,M) < or = 0.14 x 10(6) M-1, Ka(R,M) = 1.78 x 10(6) M-1, and Ka(Q,R) = 0.94 x 10(6) M-1. The binding of Q to R.M was markedly greater than that of Q to R [Ka(Q,R.M)/Ka(Q,R) > 62]. High cooperativity for this interaction occurs in either a single-site model or in lattice models for the binding of M to R. Data obtained using five other RNA 10-mers, each with the sequence altered at the AUG codon, suggest that this cooperativity is AUG dependent. The data are consistent with a scheme in which mRNA and Q bind independently to the 40S ribosome, but when the AUG codon is properly aligned with Q, a conformational change results in a 2.4 kcal/mol stabilization of the complex.

L7 ANSWER 26 OF 42 CA COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 112:193881 CA
TITLE: Role of Co-eIF-2A and **Co-eIF-2C** in mammalian peptide chain initiation
AUTHOR(S): Roy, Ananda Lal
CORPORATE SOURCE: Univ. Nebraska-Lincoln, Lincoln, NE, USA
SOURCE: (1989) 105 pp. Avail.: Univ. Microfilms Int., Order No. DA8925258
From: Diss. Abstr. Int. B 1990, 50(7), 2908-9
DOCUMENT TYPE: Dissertation
LANGUAGE: English
AB Unavailable

L7 ANSWER 27 OF 42 MEDLINE on STN DUPLICATE 18
ACCESSION NUMBER: 89166483 MEDLINE
DOCUMENT NUMBER: 89166483 PubMed ID: 3233204
TITLE: Natural mRNA is required for directing Met-tRNA(f) binding to 40S ribosomal subunits in animal cells: involvement of Co-eIF-2A in natural mRNA-directed initiation complex

formation.
AUTHOR: Roy A L; Chakrabarti D; Datta B; Hileman R E; Gupta N K
CORPORATE SOURCE: Department of Chemistry, University of Nebraska, Lincoln 68588-0304.
CONTRACT NUMBER: GM 22079 (NIGMS)
SOURCE: BIOCHEMISTRY, (1988 Oct 18) 27 (21) 8203-9.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198905
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 20000303
Entered Medline: 19890502

AB Two protein factors, eIF-2 as well as a high molecular weight protein complex from reticulocyte ribosomal high-salt wash which we term Co-eIF-2, promote Met-tRNA(f) binding to 40S ribosomes. This binding is dependent on the presence of an AUG codon or natural mRNAs [Roy et al. (1984) Biochem. Biophys. Res. Commun. 122, 1418-1425]. Co-eIF-2 contains two component activities, Co-eIF-2A and **Co-eIF-2C**. Previously, we have purified an 80-kDa polypeptide containing Co-eIF-2A activity and showed that this polypeptide is a component of Co-eIF-2 and is responsible for Co-eIF-2A activity in Co-eIF-2 [Chakravarty et al. (1985) J. Biol. Chem. 260, 6945-6949]. We now report purification of a protein complex (subunits of Mr 180K, 110K, 65K, 63K, 53K, 50K, 43K, and 40K) containing **Co-eIF-2C** activity and devoid of Co-eIF-2A activity. In SDS-PAGE, the purified **Co-eIF-2C** preparation and an eIF-3 preparation (purified in Dr. A. Wahba's laboratory) separated into seven similar major polypeptides (Mr 110K, 65K, 63K, 53K, 50K, 43K, and 40K). The 50-kDa polypeptide in **Co-eIF-2C** was immunoreactive with a monoclonal antibody against eIF-4A (50 kDa). We have studied the roles of purified Co-eIF-2A and **Co-eIF-2C** activities in ternary and Met-tRNA(f).40S ribosome complex formation. The results are as follows: (1) At low and presumably physiological factor concentration (30 nM), eIF-2 did not form detectable levels of ternary complex. Moreover, such complex formation was totally dependent on the presence of Co-eIF-2A and/or **Co-eIF-2C**. (ABSTRACT TRUNCATED AT 250 WORDS)

L7 ANSWER 28 OF 42 MEDLINE on STN DUPLICATE 19
ACCESSION NUMBER: 86059339 MEDLINE
DOCUMENT NUMBER: 86059339 PubMed ID: 3851808
TITLE: Protein synthesis in rabbit reticulocytes. A study of the mechanism of Co-eIF-2 action.
AUTHOR: Bagchi M K; Chakravarty I; Datta B; Chakrabarti D; Gupta N K
CONTRACT NUMBER: GM 22079 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1985 Dec 5) 260 (28) 14976-81.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198601
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 20000303
Entered Medline: 19860103

AB The characteristics of component activities in Co-eIF-2 (where eIF is eukaryotic initiation factor) protein complex have been studied. (i) At

limiting concentrations, Co-eIF-2 promoted rapid GDP binding to eIF-2 and also GDP displacement from eIF-2 X GDP during ternary complex formation in the presence of GTP and Mg2+ (**Co-eIF-2C** activity) but did not significantly stimulate ternary complex formation by eIF-2. (ii) At higher concentrations, Co-eIF-2 significantly enhanced ternary complex formation by eIF-2 and also rendered the complex stable to aurintricarboxylic acid presumably as Co-eIF-2 became physically bound to the ternary complex (Co-eIF-2A activity). (iii) Ternary complex preformed in the presence of Co-eIF-2 and without Mg2+ dissociated upon subsequent addition of Mg2+ (Co-eIF-2B activity). This dissociation reaction was presumably due to loss of interaction of the Co-eIF-2A component in Co-eIF-2 with the ternary complex (reversal of Co-eIF-2A activity) as the complex became increasingly sensitive to aurintricarboxylic acid with increasing Mg2+ concentration. In another study, purified eIF-2 was freed of bound GDP by treatment with alkaline phosphatase and the characteristics of native and GDP-free eIF-2 were compared. (i) One mM Mg2+ inhibited (60%) ternary complex formation by native eIF-2 but not by GDP-free eIF-2. Addition of exogenous GDP rendered GDP-free eIF-2 sensitive to Mg2+ indicating that Mg2+ inhibition is due to eIF-2-bound GDP. (ii) In the presence of Mg2+, Co-eIF-2 stimulated similarly ternary and Met-tRNAf X 40 S X AUG complex formation by both native and GDP-free eIF-2. Such stimulatory activity in each case was strongly inhibited by prior phosphorylation of eIF-2 alpha subunit by heme-regulated translational inhibitor. (iii) Ternary complexes preformed using either native and GDP-free eIF-2 and excess Co-eIF-2A80 in the absence of Mg2+ did not form Met-tRNAf X 40 S X AUG complex. They required trace amounts of Co-eIF-2 for such activity.

L7 ANSWER 29 OF 42 CA COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 103:174154 CA

TITLE: Protein synthesis in rabbit reticulocytes. A study of the mechanism of Co-eIF-2 action

AUTHOR(S): Bagchi, Milan K.; Chakravarty, Indrani; Datta, Bansidhar; Chakrabarti, Debopam; Gupta, Naba K.

CORPORATE SOURCE: Dep. Chem., Univ. Nebraska, Lincoln, NE, 68588-0304, USA

SOURCE: Journal of Biological Chemistry (1985), 260(27), 14976-81
CODEN: JBCHA3; ISSN: 0021-9258

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The characteristics of component activities in Co-eIF-2 (where eIF is eukaryotic initiation factor) protein complex were studied. At limiting concns., Co-eIF-2 promoted rapid GDP binding to eIF-2 and also GDP displacement from eIF-2.cntdot.GDP during ternary complex formation in the presence of GTP and Mg2+ (**Co-eIF-2C** activity) but did not significantly stimulate ternary complex formation by eIF-2. At higher concns., Co-eIF-2 significantly enhanced ternary complex formation by eIF-2 and also rendered the complex stable to aurintricarboxylic acid, presumably as Co-eIF-2 became phys. bound to the ternary complex (Co-eIF-2A activity). Ternary complex preformed in the presence of Co-eIF-2 without Mg2+ dissocd. upon subsequent addn. of Mg2+ (Co-eIF-2B activity). This dissocn. reaction was presumably due to loss of interaction of the Co-eIF-2A component in Co-eIF-2 with the ternary complex (reversal of Co-eIF-2A activity) as the complex became increasingly sensitive to aurintricarboxylic acid with increasing Mg2+ concn. In another study, purified eIF-2 was freed of bound GDP by treatment with alk. phosphatase and the characteristics of native and GDP-free eIF-2 were compared. Mg2+ at 1 mM inhibited (by 60%) ternary complex formation by native eIF-2 but not by GDP-free eIF-2. Addn. of exogenous GDP rendered GDP-free eIF-2 sensitive to Mg2+, indicating that Mg2+ inhibition is due to eIF-2-bound GDP. In the presence of Mg2+,

Co-eIF-2 stimulated similarly ternary and Met-tRNAf.cntdot.40 S.cntdot.AUG complex formation by both native and GDP-free eIF-2. Such stimulatory activity in each case was strongly inhibited by prior phosphorylation of eIF-2 .alpha. subunit by heme-regulated translational inhibitor. Ternary complexes preformed with either native or GDP-free eIF-2 and excess Co-eIF-2A80 in the absence of Mg2+ did not form Met-tRNA.cntdot.40 S.cntdot.AUG complex; trace amts. of Co-eIF-2 were required for such activity.

L7 ANSWER 30 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 20

ACCESSION NUMBER: 1985:376477 BIOSIS
DOCUMENT NUMBER: BA80:46469
TITLE: PROTEIN SYNTHESIS IN RABBIT RETICULOCYTES A STUDY OF THE ROLES OF EUKARYOTIC INITIATION FACTOR 2 COMPLEX 80000-MOLECULAR-WEIGHT POLYPEPTIDE AND GDP IN PEPTIDE CHAIN INITIATION.
AUTHOR(S): BAGCHI M K; CHAKRAVARTY I; AHMAD M F; NASRIN N; BANERJEE A C; OLSON C; GUPTA N K
CORPORATE SOURCE: DEP. CHEM., UNIV. NEBRASKA, LINCOLN, NEBRASKA 68588-0304.
SOURCE: J BIOL CHEM, (1985) 260 (11), 6950-6954.
CODEN: JBCHA3. ISSN: 0021-9258.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB The roles of Co-eIF-2, Co-eIF-2A80 and GDP in ternary complex and Met-tRNAf.cntdot. 40S initiation complex formation were studied. Partially purified eukaryotic initiation factor 2 (eIF-2) (50% pure) preparations contained 0.4-0.6 pmol of bound GDP/pmol of eIF-2. eIF-2 purity was calculated from ternary complex formation in the absence of Mg2+ and in the presence of excess Co-eIF-2. In the absence of Mg2+, .apprx. 30% of the potentially active eIF-2 molecules formed ternary complexes, and both Co-eIF-2 and Co-eIF-2A80 were equally effective in full activation of the eIF-2 molecules for ternary complex formation. In the presence of Mg2+, .apprx. 10% of the potentially active eIF-2 molecules formed ternary complexes in the absence of ancillary factors, and the ancillary factors Co-eIF-2A80 and Co-eIF-2 raised the incorporation to 20 and 50% of the eIF-2 molecules, respectively. In the absence of Mg2+, [3H]GDP in preformed eIF-2.cntdot.[3H]GDP was readily displaced by GTP during ternary complex formation. In the presence of Mg2+, [3H]GDP remained tightly bound to eIF-2 and ternary complex formation was inhibited. Co-eIF-2, but not Co-eIF-2A80, was effective in promoting [3H]GDP displacement and the former was more effective in promoting ternary complex formation than the latter. eIF-2.cntdot.[3H] GDP was converted to eIF-2.cntdot.[3H] GTP by incubation in the presence of nucleoside-5'-diphosphate kinase and ATP, but the eIF-2.cntdot.[3H]GTP thus, formed did not bind Met-tRNAf in the presence of Mg2+ and required exogeneous addition of Co-eIF-2 and GTP for ternary complex formation and GTP displacement. In the absence of Mg2+, the increased ternary complex formed in the presence of eIF-2.cntdot.[3H]GDP and Co-eIF-2A80 (with accompanying loss of [3H]GDP) was inactive in a subsequent reaction, which involves Met-tRNAf transfer to 40S ribosomes (in the presence of Mg2+), and required trace amounts of Co-eIF-2 for such activity. Based on the above observations, a 2-step activation of eIF-2 molecules by the Co-eIF-2 protein complex for functional ternary complex formation is suggested. One of these steps involves the Co-eIF-2A component of Co-eIF-2. This activation resulted in stimulated Met-tRNAf binding to eIF-2 and is most apparent in the absence of Mg2+ and with aged eIF-2 molecules. Another activation step involves the **Co-eIF-2C** component. In this activated state, guanine nucleotides (GDP or GTP) bound to eIF-2 are readily displaced by GTP during the formation of functional ternary complexes.

L7 ANSWER 31 OF 42 MEDLINE on STN DUPLICATE 21

ACCESSION NUMBER: 85207711 MEDLINE
DOCUMENT NUMBER: 85207711 PubMed ID: 3888988
TITLE: Protein synthesis in rabbit reticulocytes. Purification and properties of an Mr 80,000 polypeptide (Co-eIF-2A80) with Co-eIF-2A activity.
AUTHOR: Chakravarty I; Bagchi M K; Roy R; Banerjee A C; Gupta N K
CONTRACT NUMBER: GM 22079 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1985 Jun 10) 260 (11) 6945-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198507
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 20000303
Entered Medline: 19850709

AB The high molecular weight protein complex, Co-eIF-2, contains both Co-eIF-2A and **Co-eIF-2C** activities (Bagchi, M. K., Banerjee, A. C., Roy, R., Chakravarty, I., and Gupta, N. K. (1982) Nucleic Acids Res. 10, 6501-6510). Co-eIF-2A stimulated Met-tRNAf binding to eukaryotic initiation factor-2 (eIF-2) both in the presence and absence of Mg2+. **Co-eIF-2C** stimulates Met-tRNAf binding to eIF-2 in the presence of Mg2+ by relieving Mg2+ inhibition of ternary complex formation from eIF-2. Co-eIF-2 protein complex contains several polypeptides including Mr 80,000 and 50,000 polypeptides. Three polypeptides (Mr 80,000, 50,000 and 25,000) are present in 0.5 M KCl ribosomal salt wash and each possesses Co-eIF-2A activity. Mr 80,000 polypeptide (Co-eIF-2A80) has been purified to homogeneity and its properties studied. 1) Co-eIF-2A80 stimulated Met-tRNAf binding to eIF-2 and the complex formed was resistant to aurintricarboxylic acid. 2) Co-eIF-2A80 activity was N-ethylmaleimide-resistant and heat-labile; it was destroyed by heating at 55 degrees C for 4 min. 3) Antibodies prepared against homogeneous Co-eIF-2A80 strongly inhibited protein synthesis in reticulocyte lysates and, also, eIF-2 and Co-eIF-2 promoted Met-tRNAf binding to 40 S ribosomes. Inhibition of protein synthesis in reticulocyte lysates was overcome by preincubation of anti-Co-eIF-2A80 with homogeneous Co-eIF-2A80 and was partially overcome by similar preincubation with Co-eIF-2. 4) Upon limited digestion with Staphylococcus aureus V8 protease, the homogeneous Co-eIF-2A80 gave two major polypeptide fragments (Mr 50,000 and 25,000). Upon similar treatment, an Mr 80,000 polypeptide band isolated from the sodium dodecyl sulfate-gel of the Co-eIF-2 protein complex gave four major polypeptide fragments, and two of these fragments (Mr 50,000 and 25,000) were similar to those given by Co-eIF-2A80, indicating that this Mr 80,000 polypeptide band contains the Co-eIF-2A80 component. We suggest that Co-eIF-2A80 is a component of Co-eIF-2 and is also essential for Co-eIF-2 activity and overall peptide chain initiation.

L7 ANSWER 32 OF 42 MEDLINE on STN DUPLICATE 22
ACCESSION NUMBER: 83065205 MEDLINE
DOCUMENT NUMBER: 83065205 PubMed ID: 6959132
TITLE: Protein synthesis in rabbit reticulocytes: characteristics of the protein factor RF that reverses inhibition of protein synthesis in heme-deficient reticulocyte lysates.
AUTHOR: Grace M; Ralston R O; Banerjee A C; Gupta N K
CONTRACT NUMBER: 18796 (NIGMS)
GM 22079 (NCRR)
RR 07055
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1982 Nov) 79 (21) 6517-21.

Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198301
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19970203
Entered Medline: 19830127

AB During heme deficiency in reticulocyte lysates, the heme-regulated translational inhibitor of protein synthesis (HRI) is activated and shuts off protein synthesis. In partial reactions, HRI phosphorylates the Mr 38,000 subunit (alpha subunit) of eukaryotic initiation factor 2 (eIF-2), which forms a ternary complex, Met-tRNAf X eIF-2 X GTP. The eIF-2 alpha (P) thus formed is not recognized by two eIF-2 ancillary factors, Co-eIF-2B (which promotes the dissociation of the ternary complex at high Mg2+) and **Co-eIF-2C** (which reverses the inhibition of ternary complex formation), and thus, is presumably inactive in peptide chain initiation. A protein factor, designated RF, which reverses inhibition of protein synthesis in heme-deficient reticulocyte lysates, has been purified from reticulocyte cell supernatant. RF is a high molecular weight (Mr approximately equal to 450,000) protein complex composed of multiple polypeptides. An active RF preparation contains Co-eIF-2B and **Co-eIF-2C** activities, and these two activities in RF preparation are not inhibited by HRI and ATP--i.e., eIF-2 alpha (P) is recognized. During purification, RF remains associated with eIF-2 activity (eIF-2 X RF) and can be freed of this eIF-2 activity by CM-Sephadex chromatography. Both eIF-2 X RF and RF contain a Mr 38,000 polypeptide component that is indistinguishable from the Mr 38,000 subunit of eIF-2 by two-dimensional gel electrophoresis. It has been observed that a significant part of this Mr 38,000 polypeptide component in eIF-2 X RF and almost the entire Mr 38,000 polypeptide component in RF remain unphosphorylated after prolonged incubation with HRI and ATP. A possible role of this free Mr 38,000 polypeptide in RF action is discussed.

L7 ANSWER 33 OF 42 MEDLINE on STN DUPLICATE 23
ACCESSION NUMBER: 83090418 MEDLINE
DOCUMENT NUMBER: 83090418 PubMed ID: 6924750
TITLE: Protein synthesis in rabbit reticulocytes: characteristics of CO-eIF-2 protein complex.
AUTHOR: Bagchi M K; Banerjee A C; Roy R; Chakrabarty I; Gupta N K
CONTRACT NUMBER: BR 07055 (NIGMS)
GM 18796 (NIGMS)
GM 22079
SOURCE: NUCLEIC ACIDS RESEARCH, (1982 Oct 25) 10 (20) 6501-10.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198302
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 20000303
Entered Medline: 19830214

AB A high molecular weight reticulocyte protein factor, named Co-eIF-2, contains Co-eIF-2A, Co-eIF-2B, and **Co-eIF-2C** activities and stimulates Met-tRNAf binding to eIF-2 both in the presence and absence of Mg2+. Some characteristics of this stimulation in the absence of Mg2+ are: (1) Stimulation is most pronounced at low eIF-2 levels. (2) Stimulation is partially resistant to heat and NEM treatment, and thus appears to be due to the combined action of both heat and

NEM-insensitive Co-eIF-2A, and heat and NEM-sensitive **Co-eIF-2C** activities. (3) [3H]GDP bound in eIF-2 . [3H]GDP complex is rapidly displaced by unlabelled GTP during ternary complex formation Co-eIF-2 stimulates Met-tRNAf binding to eIF-2 even when added after the [3H]GDP from eIF-2 . [3H]GDP has been completely displaced. This indicates that Co-eIF-2-stimulation is not due to GDP displacement from eIF-2 . GDP. We propose that eIF-2 molecules become inactive in the presence of Mg2+ and at high dilution, and Co-eIF-2 restores the inactive eIF-2 molecules into an active form.

L7 ANSWER 34 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 24

ACCESSION NUMBER: 1982:238564 BIOSIS
DOCUMENT NUMBER: BA74:11044
TITLE: PROTEIN SYNTHESIS IN RABBIT RETICULOCYTES A STUDY OF PEPTIDE CHAIN INITIATION USING NATIVE AND BETA SUBUNIT DEPLETED EUKARYOTIC INITIATION FACTOR.
AUTHOR(S): DAS A; BAGCHI M K; GHOSH-DASTIDAR P; GUPTA N K
CORPORATE SOURCE: DEP. BIOL. SCIENCES, STANFORD UNIV., STANFORD, CALIF. 94305.
SOURCE: J BIOL CHEM, (1982) 257 (3), 1282-1288.
CODEN: JBCHA3. ISSN: 0021-9258.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Purified eukaryotic peptide chain initiation factor 2 (eIF-2) preparations contain 3 polypeptide components, .alpha., .beta. and .gamma.. A pancreatic protease treatment procedure similar to that described by Mitsui, Datta and Ochoa was used to preferentially remove the .beta.-subunit of eIF-2. The .beta.-less eIF-2 was further purified by using phosphocellulose chromatography and the activities of native and .beta.-less eIF-2 preparations were compared. The results were: both native and .beta.-less eIF-2 responded similarly to all the eIF-2 ancillary factors, Co-eIF-2A, Co-eIF-2B and **Co-eIF-2C**; addition of anti-eIF-2 preparation strongly inhibited (.apprx. 80%) protein synthesis in reticulocyte lysates and both native and .beta.-less eIF-2 restored protein synthesis activity of the anti-eIF-2-treated lysate to a similar extent (.apprx. 70%); a significant part of Met-tRNAf bound in ternary complexes, formed in the absence of Mg2+ with both native and .beta.-less eIF-2, was subsequently transferred to 40 S ribosomes upon futher addition of 40 S ribosomes, Mg2+ and AUG-codon. However, such Met-tRNAf binding to 40 S ribosomes was not inhibited by the heme-regulated eIF-2 kinase and ATP; addition of a partially purified factor preparation containing Co-eIF-2B and **Co-eIF-2C** activities in the presence of 1 mM Mg2+ stimulated significantly (8- to 12-fold) Met-tRNAf binding to 40 S ribosomes in the presence of AUG-codon with both native and .beta.-less eIF-2. Such Co-eIF-2B- and **Co-eIF-2C**-stimulated Met-tRNA.cntdot.40 S complex formation was significantly inhibited by the heme-regulated eIF-2 kinase and ATP. Under physiological Mg2+ concentration, eIF-2 and at least 1 additional protein factor preparation are probably required for efficient Met-tRNAf.cntdot.40 S AUG complex formation and both native and .beta.-less eIF-2 are likely to be active in this complex formation.

L7 ANSWER 35 OF 42 MEDLINE on STN DUPLICATE 25

ACCESSION NUMBER: 82182178 MEDLINE
DOCUMENT NUMBER: 82182178 PubMed ID: 7073685
TITLE: Protein synthesis in rabbit reticulocytes XXXI: Purification of **Co-eIF-2C** and studies of its roles in peptide chain initiation.
AUTHOR: Das A; Bagchi M; Roy R; Ghosh-Dastidar P; Gupta N K
CONTRACT NUMBER: 22079 (NIGMS)

GM 18796
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1982 Jan 15) 104 (1) 89-98.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198206
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 20000303
Entered Medline: 19820624

L7 ANSWER 36 OF 42 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 82:65791 SCISEARCH
THE GENUINE ARTICLE: NA323
TITLE: PROTEIN-SYNTHESIS IN RABBIT RETICULOCYTES .31. PURIFICATION OF **CO-EIF-2C** AND STUDIES OF ITS ROLES IN PEPTIDE-CHAIN INITIATION
AUTHOR: DAS A (Reprint); BAGCHI M; ROY R; GHOSHDASTIDAR P; GUPTA N K
CORPORATE SOURCE: STANFORD UNIV, DEPT BIOL SCI, STANFORD, CA, 94305 (Reprint); UNIV NEBRASKA, DEPT CHEM, LINCOLN, NE, 68588
COUNTRY OF AUTHOR: USA
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1982 ) Vol. 104, No. 1, pp. 89-98.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 29

L7 ANSWER 37 OF 42 CA COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 97:210516 CA
TITLE: Roles of eukaryotic initiation factor 2 ancillary factors in the regulation of eukaryotic protein synthesis initiation
AUTHOR(S): Gupta, Naba K.
CORPORATE SOURCE: Dep. Chem., Univ. Nebraska, Lincoln, NE, 68588, USA
SOURCE: Current Topics in Cellular Regulation (1982), 21, 1-33
CODEN: CTCRAE; ISSN: 0070-2137
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 88 refs. on protein formation initiation factors eIF-2, Co-eIF-2A, Co-eIF-2B, **Co-eIF-2C**, and RF and eIF-2 kinases.

L7 ANSWER 38 OF 42 MEDLINE on STN DUPLICATE 26
ACCESSION NUMBER: 81215611 MEDLINE
DOCUMENT NUMBER: 81215611 PubMed ID: 7240221
TITLE: Protein synthesis in rabbit reticulocytes. Purification and characterization of a double-stranded RNA-dependent protein synthesis inhibitor from reticulocyte lysates.
AUTHOR: Das H K; Das A; Ghosh-Dastidar P; Ralston R O; Yaghmai B; Roy R; Gupta N K
CONTRACT NUMBER: GM 18796 (NIGMS)
GM 22079 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1981 Jun 25) 256 (12) 6491-5.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 198108
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 20000303
Entered Medline: 19810820

AB Reticulocyte lysates contain a latent form of eukaryotic peptide chain initiation factor 2 (eIF-2) kinase (dsI) which becomes activated in the presence of double-stranded RNA and ATP and inhibits protein synthesis. The latent form of dsI has been partially purified from reticulocyte ribosomal salt wash. The purified dsI has been activated by incubation in the presence of poly(rI).poly(rC) and [gamma 32P]ATP and the activated dsI has been further purified to near homogeneity. Upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis, purified [32P]dsI shows an intensely staining 67,000-dalton polypeptide band which corresponds to a single 67,000-dalton radioactive band. During Sephadex (G-200) gel filtration, both the latent form of dsI and the activated dsI elute similarly with a peak corresponding to a molecular weight of 67,000. Purified dsI phosphorylates the 38,000-dalton subunit of eIF-2 and, under conditions of eIF-2 phosphorylation, dsI strongly inhibits AUG-dependent Met-tRNAf binding to 40 S ribosomes. Also, in partial reactions, eIF-2 alpha (P) formed by phosphorylation of eIF-2 using dsI and ATP, is not recognized by two eIF-2 ancillary factors, Co-eIF-2B and **Co-eIF-2C**. These results are similar to those reported previously for the heme-regulated eIF-2 kinase (Das, A., Ralston, R. O., Grace, M., Roy, R., Ghosh-Dastidar, P., Das H. K., Yaghmai, B., Palmieri, S., and Gupta, N. K. (1979) Proc. Natl. Acad. Sci. U. S. A. 76,5076-5079) and suggest that dsI, like the heme-regulated eIF-2 kinase phosphorylates eIF-2 and eIF-2 alpha (P) thus formed, in both cases, is not recognized by Co-eIF-2B and **Co-eIF-2C**, and is inactive in some step(s) of Met-tRNAf.40 S initiation complex formation.

L7 ANSWER 39 OF 42 MEDLINE on STN DUPLICATE 27
ACCESSION NUMBER: 81191851 MEDLINE
DOCUMENT NUMBER: 81191851 PubMed ID: 6153053
TITLE: Protein synthesis in rabbit reticulocytes. Co-eIF-2A reverses mRNA inhibition of ternary complex (Met-tRNAf.eIF-2.GTP) formation by eIF-2.
AUTHOR: Roy R; Ghosh-Dastidar P; Das A; Yaghmai B; Gupta N K
CONTRACT NUMBER: GM 18796 (NIGMS)
GM 22079 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1981 May 25) 256 (10) 4719-22.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198107
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 20000303
Entered Medline: 19810720

AB mRNAs, at low concentrations, drastically inhibit ternary complex formation by eIF-2 (Met-tRNAf.eIF-2.GTP) and, when added to the preformed ternary complex, cause extensive dissociation of the complex. Co-eIF-2A stimulates (2- to 4-fold) Met-tRNAf binding to eIF-2 and, in the presence of excess Co-eIF-2A, the stimulated Met-tRNAf binding to eIF-2 is fully resistant to mRNAs. Other cofactors tested such as Co-eIF-2B and **Co-eIF-2C** do not reverse mRNA inhibition of ternary complex formation.

L7 ANSWER 40 OF 42 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1981:241854 BIOSIS
DOCUMENT NUMBER: BA72:26838
TITLE: EYESPOT DISEASE OF SUGARCANE SACCHARUM-OFFICINARUM INDUCTION OF HOST SPECIFIC TOXIN AND ITS INTERACTION WITH LEAF CELLS.
AUTHOR(S): LARKIN P J; SCOWCROFT W R
CORPORATE SOURCE: DIV. PLANT IND., COMMONW. SCI. IND. RES. ORGAN., P.O. BOX 1600, CANBERRA, A.C.T. 2601, AUST.
SOURCE: PLANT PHYSIOL (BETHESDA), (1981) 67 (3), 408-414.
CODEN: PLPHAY. ISSN: 0032-0889.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB helminthosporium sacchari produces a toxin which is responsible for the symptoms of eyespot disease in S. officinarum [sugarcane cultivars Q47, **Q99**, and Q101]. A rapid and highly repeatable bioassay based on increase in conductivity of tissue leachastes showed that the interaction of toxin with sugarcane obeys Michaelis-Menten hyperbolic saturation kinetics. There was no evidence for positive or negative cooperation interaction. Resistant and susceptible cultivars of sugarcane had distinctive conductivity characteristics. Co-cultures of H. sacchari and suspension cultures of sugarcane gave up to a 4000-fold increase in toxin production.

L7 ANSWER 41 OF 42 MEDLINE on STN DUPLICATE 28
ACCESSION NUMBER: 80182264 MEDLINE
DOCUMENT NUMBER: 80182264 PubMed ID: 7372648
TITLE: Protein synthesis in rabbit reticulocytes. A study of the mechanism of interreaction of fluorescently labeled co-eIF-2A with eIF-2 using fluorescence polarization.
AUTHOR: Ghosh-Dastidar P; Giblin D; Yaghmai B; Das A; Das H K; Parkhurst L J; Gupta N K
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1980 May 10) 255 (9) 3826-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198007
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 20000303
Entered Medline: 19800722
AB 5-Dimethylaminonaphthalene-1-sulfonyl (dansyl)-Co-eIF-2A was prepared using homogeneous Co-eIF-2A. Dansyl-Co-eIF-2A was as active as untreated Co-eIF-2A when assayed for stimulation of ternary complex formation and also for protection of the ternary complex from dissociation by aurintricarboxylic acid. The mechanism of interaction of dansyl-Co-eIF-2A with eIF-2 was studied by measuring changes in fluorescence polarization. These studies indicate that dansyl-Co-eIF-2A interacts specifically with the ternary complex and does not interact with free eIF-2 or with two other high molecular weight protein complexes, Co-eIF-2B and **Co-eIF-2C**. Mg2+ inhibits ternary complex formation by eIF-2 and **Co-eIF-2C** relieves this Mg2+ inhibition of ternary complex formation. In both cases, the changes in fluorescence polarization of dansyl-Co-eIF-2A correlate well with the extent of ternary complex formed.

L7 ANSWER 42 OF 42 MEDLINE on STN DUPLICATE 29
ACCESSION NUMBER: 80056637 MEDLINE
DOCUMENT NUMBER: 80056637 PubMed ID: 291924
TITLE: Protein synthesis in rabbit reticulocytes: mechanism of protein synthesis inhibition by heme-regulated inhibitor.

AUTHOR: Das A; Ralston R O; Grace M; Roy R; Ghosh-Dastidar P; Das H K; Yaghmai B; Palmieri S; Gupta N K
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1979 Oct) 76 (10) 5076-9. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198001
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19970203
Entered Medline: 19800128

AB Partially purified Met-tRNAf binding factor, eIF-2, was phosphorylated by using heme-regulated inhibitor (HRI). Phosphorylated eIF-2 was freed from HRI by phosphocellulose column chromatography. Analysis by isoelectric focusing showed 100% phosphorylation of the 38,000-dalton subunit of eIF-2. Both eIF-2 and eIF-2(P) formed ternary complexes with Met-tRNAf and GTP with almost the same efficiency, and in both cases the ternary complex formation was drastically inhibited by prior addition of Mg2+. However, whereas the ternary complexes formed with eIF-2 could be stimulated by **Co-eIF-2C** at 1 mM Mg2+ and dissociated by Co-eIF-2B at 5 mM Mg2+, the ternary complexes formed with eIF-2(P) were unresponsive to both Co-eIF-2B and Co-e-IF-2C. Also, under conditions of eIF-2 phosphorylation, HRI drastically inhibited AUG-dependent Met-tRNAf binding to 40S ribosomes. However, HRI (in the presence of ATP) had no effect on the joining of preformed Met-tRNAf . 40S . AUG complex to the 60S ribosomal subunit to form Met-tRNAf-80S . AUG complex. These studies suggest that HRI inhibits protein synthesis initiation by phosphorylation of the 38,000-dalton subunit of eIF-2. HRI-phosphorylated eIF-2 does not interact with at least two other protein factors, Co-eIF-2B and **Co-eIF-2C**, and is thus inactive in protein synthesis initiation.

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(FILE 'HOME' ENTERED AT 12:31:12 ON 16 AUG 2003)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 12:31:17 ON 16 AUG 2003

L1 107 S (EUKARYOT? (N) TRANSLATION? (N) FACTOR (N) 2C?) OR (CO (N) EI
L2 130563 S ANTISENSE OR RNAI OR (ANTI (N) SENSE) OR (COMPLEMENT? (2N) (O
L3 16 S L1 AND L2
L4 6 DUP REM L3 (10 DUPLICATES REMOVED)
L5 8 S L1 (3N) INHIB?
L6 3 DUP REM L5 (5 DUPLICATES REMOVED)
L7 42 DUP REM L1 (65 DUPLICATES REMOVED)

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     FILE 'BIOSIS, MEDLINE, SCISEARCH, CA' ENTERED AT 08:41:51 ON 03 MAY 2002
L1          7142 S EIF2? OR CO-EIF? OR (EUKARYOTIC (3N) INITIATION (3N) FACTOR)
L2         81699 S ANTISENSE OR (COMPLEMENT? (3N) (SEAUENC? OR OLIGO?))
L3            83 S L1 AND L2
L4             2 S L3 AND (INHIB? OR REDUC? OR PREVENT? OR LOWER? OR SUPPRESS?)
L5        127625 S ANTISENSE OR (COMPLEMENT? (3N) (SEQUENC? OR OLIGO?))
L6           150 S L1 AND L5
L7             2 S L6 AND (INHIB? OR REDUC? OR PREVENT? OR LOWER? OR SUPPRESS?)
L8          7511 S WARD, D?/AU
L9         49781 S L8 AND ANTISENSE OR (COMPLEMENT? (3N) (SEQUENC? OR OLIGO))
L10           45 S L8 AND (ANTISENSE OR (COMPLEMENT? (3N) (SEQUENC? OR OLIGO)))
L11            0 S L10 AND (EIF2? OR (EUKARYOTIC TRANSCRIPTION FACTOR))

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